

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:21:40 ; Search time 103.591 Seconds  
(without alignments)  
1241.024 Million cell updates/sec

Title: US-10-021-121-2  
Perfect score: 2450  
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2450	100.0	455	2	AAW33698	Aaw33698 AL-2-long
2	1841	75.1	340	2	AAW31544	Aaw31544 Human cyt
3	1841	75.1	340	2	AAW33699	Aaw33699 AL-2-shor
4	1841	75.1	340	2	AAW10637	Aaw10637 NLERK2 li
5	1841	75.1	340	6	ABU07845	Abu07845 Human eph
6	1835	74.9	340	2	AAW17081	Aaw17081 EPH famil
7	1827	74.6	340	2	AAW46615	Aaw46615 Human tra
8	1771	72.3	340	6	ABU07846	Abu07846 Mouse eph
9	628.5	25.7	334	2	AAW00287	Aaw00287 Mouse Eph

10	628.5	25.7	336	2	AAR92742	Aar92742	Murine he
11	626.5	25.6	336	6	ABU07844	Abu07844	Mouse eph
12	623	25.4	346	2	AAR55059	Aar55059	Elk tyros
13	623	25.4	346	2	AAR91930	Aar91930	Human cyt
14	623	25.4	346	2	AAW19249	Aaw19249	Human elk
15	623	25.4	346	2	AAW36055	Aaw36055	Human elk
16	623	25.4	346	2	AAW44323	Aaw44323	Human elk
17	623	25.4	346	6	ABU07841	Abu07841	Human eph
18	623	25.4	346	7	ABU62401	Abu62401	Human elk
19	622	25.4	346	2	AAR82606	Aar82606	Eph trans
20	621.5	25.4	331	2	AAW00288	Aaw00288	Chicken E
21	620.5	25.3	333	2	AAR94655	Aar94655	Ligand fo
22	620.5	25.3	333	2	AAR92743	Aar92743	Human hep
23	620.5	25.3	333	2	AAR89287	Aar89287	Human LER
24	620.5	25.3	333	2	AAW06337	Aaw06337	Full leng
25	620.5	25.3	333	2	AAW11308	Aaw11308	Receptor-
26	620.5	25.3	333	6	ABU07886	Abu07886	Novel hum
27	620.5	25.3	333	7	ADD89059	Add89059	TAT245. 1
28	610.5	24.9	308	2	AAR94656	Aar94656	Ligand fo
29	610.5	24.9	308	2	AAW06334	Aaw06334	Ligand #2
30	604.5	24.7	345	6	ABU07842	Abu07842	Mouse eph
31	483	19.7	89	3	AA71438	Aay71438	Human eph
32	458.5	18.7	658	3	AA796782	Aay96782	Ephrin-B2
33	456	18.6	254	6	ABU07843	Abu07843	Human eph
34	454	18.5	683	3	AA796781	Aay96781	Ephrin-B1
35	447	18.2	229	5	AAE24019	Aae24019	Murine ep
36	443	18.1	229	5	AAE24020	Aae24020	Human eph
37	431.5	17.6	195	2	AAW06333	Aaw06333	Ligand #1
38	431.5	17.6	195	2	AAW11307	Aaw11307	Receptor-
39	284.5	11.6	92	4	AAM37671	Aam37671	Peptide #
40	284.5	11.6	92	5	ABG46524	Abg46524	Human pep
41	196.5	8.0	136	4	AAM37534	Aam37534	Peptide #
42	196.5	8.0	136	5	ABG46394	Abg46394	Human pep
43	195	8.0	82	3	AA71437	Aay71437	Human eph
44	193.5	7.9	106	3	AAB54187	Aab54187	Human pan
45	192	7.8	82	3	AA71436	Aay71436	Human eph

# ALIGNMENTS

## RESULT 1

AAW33698

ID AAW33698 standard; protein; 455 AA.

XX

AC AAW33698;

XX

DT 30-APR-1998 (first entry)

XX

DE AL-2-long (AL-21) protein.

XX

KW AL-21; AL-2; AL-2-long; human; treatment; neurological disorder; tumour;  
 KW rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;  
 KW psoriasis; Alzheimer's disease; epilepsy.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .26
FT		/note= "signal peptide"
FT	Protein	27. .455
FT		/note= "mature protein"
FT	Domain	27. .219
FT		/note= "extracellular domain"
FT	Domain	220. .245
FT		/note= "hydrophobic transmembrane domain"
XX		
PN	WO9740153-A1.	
XX		
PD	30-OCT-1997.	
XX		
PF	17-APR-1997; 97WO-US006345.	
XX		
PR	19-APR-1996; 96US-00635130.	
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Caras IW;	
XX		
DR	WPI; 1997-535837/49.	
DR	N-PSDB; AAV06354.	
XX		
PT	Human AL-2 neurotrophic factor and related DNA - used to develop products	
PT	for, e.g. treating neurologic disorders, angiogenesis disorders, tumours	
PT	or rheumatoid arthritis or for wound healing.	
XX		
PS	Claim 20; Fig 1A-C; 86pp; English.	
XX		
CC	This is a AL-2-long (AL-2l) protein. The AL-2 is a novel Eph-related	
CC	tyrosine kinase receptor ligand. AL-2 can be administered to patients in	
CC	whom the nervous system has been damaged by trauma, surgery, stroke,	
CC	ischaemia, infection, metabolic disease, nutritional deficiency,	
CC	malignancy, or toxic agents, to promote the survival or growth of	
CC	neurons. They can be used to treat motoneuron disorders such as	
CC	amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and	
CC	various conditions involving spinal muscular atrophy, or paralysis. AL-2	
CC	can be used to treat human neurodegenerative disorders, such as	
CC	Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating	
CC	diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,	
CC	nerve deafness, Menier's disease, and other disorders of the cerebellum.	
CC	AL-2 can be used as cognitive enhancer, to enhance learning particularly	
CC	in dementias or trauma, since they can promote axonal outgrowth and	
CC	synaptic plasticity, particularly of hippocampal neurons that express AL-	
CC	2 binding Eph-family receptors and cortical neurons that express AL-2. AL	
CC	-2 can also be used for wound healing, i.e. accelerating	
CC	neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids	
CC	are useful in preparing antibodies that specifically bind to the AL-2	
CC	protein. The antibodies and the AL-2 antagonists are useful in diagnosing	
CC	and treating various neuronal disorders. AL-2 antagonists can be used for	
CC	modulating angiogenesis. They can also be used for the treatment of	
CC	tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),	
CC	myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular	
CC	glaucoma, psoriasis and rheumatoid arthritis	
XX		

SQ Sequence 455 AA;

Query Match 100.0%; Score 2450; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 2.1e-197;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

QY     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLTCDRDLRFTIKFQEY 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLTCDRDLRFTIKFQEY 120

QY    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
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Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

QY    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

QY    241 GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300

QY    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYTSISVLEWPILHTIQLFFMRSK 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYTSISVLEWPILHTIQLFFMRSK 360

QY    361 CSRVTTFLEFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CSRVTTFLEFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420

QY    421 VLVLILLLLGRLNMHQTTLLRQRASVEAEAGQHGPL 455
      ||||||||||||||||||||||||||||||||||||
Db    421 VLVLILLLLGRLNMHQTTLLRQRASVEAEAGQHGPL 455
```

RESULT 2

AAW31544

ID AAW31544 standard; protein; 340 AA.

XX

AC AAW31544;

XX

DT 14-APR-1998 (first entry)

XX

DE Human cytokine Lerk-8.

XX

KW Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase; ligand;

KW neurodegenerative disease; wound healing; neovascularisation; diagnosis;

KW therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .27

FT /label= Sig\_peptide  
 FT Protein 28. .340  
 FT /label= Mat\_protein  
 FT Domain 28. .224  
 FT /note= "extracellular domain"  
 FT Modified-site 210. .212  
 FT /note= "N-glycosylated"  
 FT Domain 225. .251  
 FT /note= "transmembrane domain"  
 FT Domain 252. .340  
 FT /note= "cytoplasmic domain"  
 FT Misc-difference 325  
 FT /note= "residue 325 is Leu in Lerk-8 variant"  
 XX  
 PN WO9736919-A2.  
 XX  
 PD 09-OCT-1997.  
 XX  
 PF 19-MAR-1997; 97WO-US004533.  
 XX  
 PR 21-MAR-1996; 96US-00621146.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Cerretti DP;  
 XX  
 DR WPI; 1997-503043/46.  
 DR N-PSDB; AAT89519.  
 XX  
 PT New isolated cytokine, Lerk-8 - binds to the hek and elk receptor  
 PT tyrosine kinases, used to develop products for diagnosis and therapy.  
 XX  
 PS Claim 3; Page 32-33; 37pp; English.  
 XX  
 CC This protein sequence comprises a novel human cytokine designated Lerk-8.  
 CC The amino acid sequence was deduced from a human foetal brain cDNA clone  
 CC (see AAT89519). Lerk-8 binds to the cell surface receptors hek and elk,  
 CC which are members of the eph/elk family of receptor tyrosine kinases.  
 CC Lerk-8 polypeptides, especially soluble polypeptides comprising amino  
 CC acid residues -27 to 142-197 of the full-length protein, can be expressed  
 CC in transformed host cells. These polypeptides can be used to purify hek  
 CC or elk proteins, and to purify or identify cells that express hek or elk  
 CC on the surface. Such cells can be used in various in vitro studies or in  
 CC vivo procedures, e.g. neural cells expressing elk can be administered to  
 CC a mammal afflicted with a neurodegenerative disorder. The Lerk-8  
 CC polypeptides can also be used to deliver diagnostic or therapeutic agents  
 CC to these cells (e.g. leukaemia cells). The Lerk-8 DNA and polypeptides  
 CC can also be used to: treat disorders mediated by defective or  
 CC insufficient amounts of Lerk-8; to treat disorders such as injury to  
 CC neural tissue or neurologic disease; to promote angiogenesis; and for  
 CC wound healing or stimulating neovascularisation of grafted tissues  
 XX  
 SQ Sequence 340 AA;

Query Match 75.1%; Score 1841; DB 2; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-146;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 60  
 |||  
 Db 1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 60  
 QY 61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQEY 120  
 |||  
 Db 61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQEY 120  
 QY 121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180  
 |||  
 Db 121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180  
 QY 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240  
 |||  
 Db 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240  
 QY 241 GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300  
 |||  
 Db 241 GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300  
 QY 301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338  
 |||  
 Db 301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338

RESULT 3

AAW33699

ID AAW33699 standard; protein; 340 AA.

XX

AC AAW33699;

XX

DT 30-APR-1998 (first entry)

XX

DE AL-2-short (AL-2s) protein.

XX

KW AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour;  
 KW rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;  
 KW psoriasis; Alzheimer's disease; epilepsy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .26

FT /note= "signal peptide"

FT Protein 27. .340

FT /note= "mature protein"

FT Domain 27. .219

FT /note= "extracellular domain"

FT Domain 220. .245

FT /note= "hydrophobic transmembrane domain"

XX

PN WO9740153-A1.

XX

PD 30-OCT-1997.

XX

PF 17-APR-1997; 97WO-US006345.

XX  
 PR 19-APR-1996; 96US-00635130.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Caras IW;  
 XX  
 DR WPI; 1997-535837/49.  
 DR N-PSDB; AAV06355.  
 XX  
 PT Human AL-2 neurotrophic factor and related DNA - used to develop products  
 PT for, e.g. treating neurologic disorders, angiogenesis disorders, tumours  
 PT or rheumatoid arthritis or for wound healing.  
 XX  
 PS Claim 20; Fig 2A-B; 86pp; English.  
 XX  
 CC This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Eph-related  
 CC tyrosine kinase receptor ligand. AL-2 can be administered to patients in  
 CC whom the nervous system has been damaged by trauma, surgery, stroke,  
 CC ischaemia, infection, metabolic disease, nutritional deficiency,  
 CC malignancy, or toxic agents, to promote the survival or growth of  
 CC neurons. They can be used to treat motoneuron disorders such as  
 CC amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and  
 CC various conditions involving spinal muscular atrophy, or paralysis. AL-2  
 CC can be used to treat human neurodegenerative disorders, such as  
 CC Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating  
 CC diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,  
 CC nerve deafness, Menier's disease, and other disorders of the cerebellum.  
 CC AL-2 can be used as cognitive enhancer, to enhance learning particularly  
 CC in dementias or trauma, since they can promote axonal outgrowth and  
 CC synaptic plasticity, particularly of hippocampal neurons that express AL-  
 CC 2 binding Eph-family receptors and cortical neurons that express AL-2. AL  
 CC -2 can also be used for wound healing, i.e. accelerating  
 CC neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids  
 CC are useful in preparing antibodies that specifically bind to the AL-2  
 CC protein. The antibodies and the AL-2 antagonists are useful in diagnosing  
 CC and treating various neuronal disorders. AL-2 antagonists can be used for  
 CC modulating angiogenesis. They can also be used for the treatment of  
 CC tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),  
 CC myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular  
 CC glaucoma, psoriasis and rheumatoid arthritis  
 XX  
 SQ Sequence 340 AA;

Query Match 75.1%; Score 1841; DB 2; Length 340;

Best Local Similarity 100.0%; Pred. No. 2.4e-146;

Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWN	SANKRFQAEGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGR	RCEAPPAPNLLLTCDRDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGR	RCEAPPAPNLLLTCDRDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLES	LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180

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      |||
Db      121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
      |||
Qy      181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      |||
Db      181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      |||
Qy      241 GVAGAGGAMCWRRRRRAKPSES RHPGPSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300
      |||
Db      241 GVAGAGGAMCWRRRRRAKPSES RHPGPSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300
      |||
Qy      301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
      |||
Db      301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338

```

RESULT 4

AAW10637

ID AAW10637 standard; protein; 340 AA.

XX

AC AAW10637;

XX

DT 23-JUN-1997 (first entry)

XX

DE NLERK2 ligand for eph-related kinase.

XX

KW LERK; ligand for eph-related kinase; ERK; NLERK2;

KW receptor protein tyrosine kinase; cell proliferation;

KW cell differentiation; cell survival; nerve cell.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .29
----	---------	--------

FT		/label= Sig_peptide
----	--	---------------------

FT	Protein	30. .340
----	---------	----------

FT		/label= Mat_protein
----	--	---------------------

FT	Modified-site	210
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FT		/label= N-glycosylation_site
----	--	------------------------------

FT	Domain	227. .251
----	--------	-----------

FT		/label= Transmembrane_domain
----	--	------------------------------

XX

PN WO9704091-A1.

XX

PD 06-FEB-1997.

XX

PF 19-JUL-1996; 96WO-AU000460.

XX

PR 20-JUL-1995; 95AU-00004263.

PR 27-NOV-1995; 95AU-00006847.

PR 22-DEC-1995; 95AU-00007299.

PR 05-FEB-1996; 96AU-00007890.

XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX

PI Nicola NA;

XX



DR WPI; 1997-132632/12.  
 DR N-PSDB; AAT60966.  
 XX  
 PT Nucleic acid mol. encoding ligand for eph-related kinase - useful for  
 PT treatment of, pref. neuronal, cells to increase survival, proliferation  
 PT and differentiation.  
 XX  
 PS Claim 16; Page 37-39; 71pp; English.  
 XX  
 CC A novel human ligand for eph-related kinase (LERK) is designated NLERK2  
 CC (AAW10637). It is encoded by a cDNA clone (AAT60966) obtd. from a human  
 CC foetal brain cDNA library. The novel receptor ligand can be expressed in  
 CC transformed host cells and used in methods for regulating the  
 CC development, maintenance or regeneration of different cells (e.g.  
 CC neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be  
 CC used to treat injury, disease or abnormality in the nervous system, and  
 CC membrane-bound NLERK2 to modulate proliferation, different or survival  
 CC e.g. in grafting procedures or transplantation. NLERK2 can also be used  
 CC to raise antibodies for use in immunotherapy, and to detect anti-NLERK2  
 CC antibodies that may occur in some autoimmune diseases  
 XX  
 SQ Sequence 340 AA;

Query Match 75.1%; Score 1841; DB 2; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-146;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
          |||
Db      1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRDLRFTIKFQ EY 120
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Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPS ESRHPGPGSFGRGGS LGLGGGGMGMPREAE PGELGIALRGG 300
          |||
Db    241 GVAGAGGAMCWRRRRRAKPS ESRHPGPGSFGRGGS LGLGGGGMGMPREAE PGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP PNIIY 338
          |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP PNIIY 338

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RESULT 5  
 ABU07845  
 ID ABU07845 standard; protein; 340 AA.  
 XX  
 AC ABU07845;

XX  
 DT 10-MAY-2003 (first entry)  
 XX  
 DE Human ephrin-B3 ligand.  
 XX  
 KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;  
 KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;  
 KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;  
 KW cell migration disorder; cell proliferation disorder; neovascularisation;  
 KW ischaemia; infarction; tissue graft; transplant; human; ephrin-B3;  
 KW tie receptor tyrosine kinase; Eph receptor ligand.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003004529-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PF 02-JUL-2002; 2002WO-IB002524.  
 XX  
 PR 02-JUL-2001; 2001US-0302960P.  
 XX  
 PA (LICN ) LICENTIA LTD.  
 XX  
 PI Alitalo K, Kubo H;  
 XX  
 DR WPI; 2003-210341/20.  
 DR N-PSDB; ABX12546.  
 XX  
 PT Identifying modulators of binding between a Tie receptor tyrosine kinase  
 PT and an Ephrin ligand, useful for promoting neovascularization, comprises  
 PT contacting a Tie receptor with an Ephrin in the presence of a putative  
 PT modulator.  
 XX  
 PS Disclosure; Page 117-119; 199pp; English.  
 XX  
 CC The invention describes a method of identifying a modulator of binding  
 CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method  
 CC comprises contacting a Tie receptor composition with an Ephrin  
 CC composition in the presence and in the absence of a putative modulator  
 CC compound, and detecting the binding between Tie receptor and the Ephrin  
 CC in the presence and in the absence of the putative modulator. The method  
 CC is useful for identifying a modulator of binding between a Tie receptor  
 CC tyrosine kinase and an Ephrin ligand. Modulators identified from the  
 CC method are useful in modulating angiogenic processes, including  
 CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-  
 CC Tie biology, aberrant growth, migration or proliferation of cells that  
 CC express a Tie receptor, or for promoting growth of vessel or  
 CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or  
 CC chronic compound, or a tissue graft or transplant). This is the amino  
 CC acid sequence of human Ephrin-B3, a member of the Ephrin-B subclass of  
 CC ligands that are bound to the membrane via a transmembrane domain and  
 CC short cytoplasmic tail and function as Eph receptor ligands  
 XX  
 SQ Sequence 340 AA;

Query Match

75.1%; Score 1841; DB 6; Length 340;

Best Local Similarity 100.0%; Pred. No. 2.4e-146;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60
      |||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
      |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
      |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300
      |||
Db    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
      |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 6

AAW17081

ID AAW17081 standard; protein; 340 AA.

XX

AC AAW17081;

XX

DT 09-AUG-1997 (first entry)

XX

DE EPH family ligand Efl-6.

XX

KW Efl-6; Eph; Elk; receptor tyrosine kinase; signal transduction; ligand;  
KW neurological disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .24

FT /label= Sig\_peptide

FT Protein 25. .340

FT /label= Mat\_protein

FT Misc-difference 166

FT /label= Gln, Arg

FT Domain 225. .249

FT /label= Transmembrane\_domain

XX

PN W09715667-A1.

XX

PD 01-MAY-1997.

XX

PF 25-OCT-1996; 96WO-US017201.  
 XX  
 PR 25-OCT-1995; 95US-0007015P.  
 XX  
 PA (REGE-) REGENERON PHARM INC.  
 XX  
 PI Davis S, Gale NW, Yancopoulos GD;  
 XX  
 DR WPI; 1997-259021/23.  
 DR N-PSDB; AAT69808.  
 XX  
 PT New nucleic acid encoding Efl-6 ligand protein - used for promoting  
 PT growth and proliferation of neuronal cells and in drug screening.  
 XX  
 PS Claim 2; Fig 1; 36pp; English.  
 XX  
 CC A novel ligand (AAW17081), designated Efl-6 (or Eph transmembrane  
 CC tyrosine kinase family ligand 6), binds to the Elk, Nuk/Cek5, Hek2/Sek4,  
 CC Htk and Sek1 receptors on cells. Its amino acid sequence was deduced from  
 CC a human frontal cortex cDNA clone (AAT69808). Recombinant Elf-6,  
 CC truncated soluble polypeptides comprising the extracellular domain of Elf  
 CC -6, and Efl-6 ligandbodies comprising soluble Efl-6 and the Fc portion of  
 CC IgG can be expressed in host cells. These can be used to support neuronal  
 CC and other Eph receptor-bearing cell populations for treatment of  
 CC neurological disorders, in drug screening and to raise diagnostic  
 CC antibodies  
 XX  
 SQ Sequence 340 AA;

Query Match 74.9%; Score 1835; DB 2; Length 340;  
 Best Local Similarity 99.7%; Pred. No. 7.8e-146;  
 Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLXVGQSPRGGAVPRKP	180
Qy	181	VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Qy	241	GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGMPREAE PGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGMPREAE PGELGIALRGG	300
Qy	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY	338
Db	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY	338

RESULT 7

AAW46615

ID AAW46615 standard; protein; 340 AA.

XX

AC AAW46615;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human transmembrane ligand Elk-L3.

XX

KW Elk-L3; Elk-related receptor tyrosine kinase; transmembrane ligand;

KW human; signal transduction; axonogenesis; nerve cell; neurone;

KW Alzheimer's disease; Parkinson's disease; Huntingdon's disease;

KW demyelination; multiple sclerosis; amyotrophic lateral sclerosis;

KW nervous system infection; Wernicke's disease; trauma; ischaemia; stroke;

KW nutritional polyneuropathy; progressive supranuclear palsy;

KW Shy Drager's syndrome; multistem degeneration;

KW olivo ponto cerebellar atrophy, peripheral nerve damage.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 166

FT /label= Gln, Arg

FT Domain 225..249

FT /note= "transmembrane domain"

XX

PN WO9801548-A1.

XX

PD 15-JAN-1998.

XX

PF 04-JUL-1997; 97WO-CA000473.

XX

PR 05-JUL-1996; 96US-0021272P.

XX

PA (MOUN ) MOUNT SINAI HOSPITAL CORP.

XX

PI Holland S, Mbamalu G, Pawson T;

XX

DR WPI; 1998-101047/09.

DR N-PSDB; AAV16097.

XX

PT Modulating transmembrane ligand for an Elk-related receptor tyrosine

PT kinase - by formation of a complex between an oligomerised Elk-related

PT receptor tyrosine kinase and a transmembrane ligand.

XX

PS Disclosure; Fig 5A; 40pp; English.

XX

CC This polypeptide comprises human Elk-L3, a transmembrane ligand of Elk-

CC related receptor tyrosine kinase (ERRTK). A novel method of modulating

CC the biological activity of, or for affecting a pathway regulated by, a

CC transmembrane ligand for an ERRTK in a cell expressing the transmembrane

CC ligand comprises forming a complex between a purified and isolated

CC oligomerised ERRTK, or an isoform or an extracellular domain of the

CC ERRTK, and the transmembrane ligand expressed on the cell. The complex

CC can also be used for evaluating a substance for its ability to modulate

CC the biological activity of a transmembrane ligand for an ERRTK, and to  
 CC identify substances that affect or modulate a pathway regulated by a  
 CC ERRTK. A purified and isolated oligomerised ERRTK can be used in the  
 CC preparation of a medicament for modulating neuronal development or  
 CC regeneration in a subject, or in a medicament for modulating axonogenesis  
 CC in a subject (all claimed). The substances identified by the methods can  
 CC be used to modulate axonogenesis, nerve cell interactions and  
 CC regeneration, to treat diseases and conditions involving trauma and  
 CC injury to the nervous system, such as Alzheimer's disease, Parkinson's  
 CC disease, Huntingdon's disease, demyelinating diseases, such as multiple  
 CC sclerosis, amyotrophic lateral sclerosis, bacterial and viral infections  
 CC of the nervous system, deficiency diseases, such as Wernicke's disease  
 CC and nutritional polyneuropathy, progressive supranuclear palsy, Shy  
 CC Drager's syndrome, multistem degeneration and olivo ponto cerebellar  
 CC atrophy, peripheral nerve damage, trauma, and ischaemia resulting from  
 CC stroke

XX

SQ Sequence 340 AA;

Query Match 74.6%; Score 1827; DB 2; Length 340;  
 Best Local Similarity 99.4%; Pred. No. 3.7e-145;  
 Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLXVGQSPRGGAVPRKP	180
Qy	181	VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Qy	241	GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG	300
Qy	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY	338
Db	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPQNIY	338

RESULT 8

ABU07846

ID ABU07846 standard; protein; 340 AA.

XX

AC ABU07846;

XX

DT 10-MAY-2003 (first entry)

XX

DE Mouse ephrin-B3 ligand.

XX  
 KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;  
 KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;  
 KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;  
 KW cell migration disorder; cell proliferation disorder; neovascularisation;  
 KW ischaemia; infarction; tissue graft; transplant; mouse; ephrin-B3;  
 KW tie receptor tyrosine kinase; Eph receptor ligand.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003004529-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PF 02-JUL-2002; 2002WO-IB002524.  
 XX  
 PR 02-JUL-2001; 2001US-0302960P.  
 XX  
 PA (LICN ) LICENTIA LTD.  
 XX  
 PI Alitalo K, Kubo H;  
 XX  
 DR WPI; 2003-210341/20.  
 DR N-PSDB; ABX12547.  
 XX  
 PT Identifying modulators of binding between a Tie receptor tyrosine kinase  
 PT and an Ephrin ligand, useful for promoting neovascularization, comprises  
 PT contacting a Tie receptor with an Ephrin in the presence of a putative  
 PT modulator.  
 XX  
 PS Disclosure; Page 121-122; 199pp; English.  
 XX  
 CC The invention describes a method of identifying a modulator of binding  
 CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method  
 CC comprises contacting a Tie receptor composition with an Ephrin  
 CC composition in the presence and in the absence of a putative modulator  
 CC compound, and detecting the binding between Tie receptor and the Ephrin  
 CC in the presence and in the absence of the putative modulator. The method  
 CC is useful for identifying a modulator of binding between a Tie receptor  
 CC tyrosine kinase and an Ephrin ligand. Modulators identified from the  
 CC method are useful in modulating angiogenic processes, including  
 CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-  
 CC Tie biology, aberrant growth, migration or proliferation of cells that  
 CC express a Tie receptor, or for promoting growth of vessel or  
 CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or  
 CC chronic compound, or a tissue graft or transplant). This is the amino  
 CC acid sequence of mouse Ephrin-B3, a member of the Ephrin-B subclass of  
 CC ligands that are bound to the membrane via a transmembrane domain and  
 CC short cytoplasmic tail and function as Eph receptor ligands  
 XX  
 SQ Sequence 340 AA;

Query Match 72.3%; Score 1771; DB 6; Length 340;  
 Best Local Similarity 95.6%; Pred. No. 1.9e-140;  
 Matches 323; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60







XX  
 DT 21-MAY-1996 (first entry)  
 XX  
 DE Murine hepatoma transmembrane kinase receptor ligand.  
 XX  
 KW Hepatoma transmembrane kinase; Htk; receptor; ligand; tyrosine kinase;  
 KW neurodegenerative disease.  
 XX  
 OS Mus musculus.  
 XX  
 PN W09602645-A2.  
 XX  
 PD 01-FEB-1996.  
 XX  
 PF 14-JUL-1995; 95WO-US008812.  
 XX  
 PR 20-JUL-1994; 94US-00277722.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Bennett BD, Matthews W;  
 XX  
 DR WPI; 1996-105907/11.  
 DR N-PSDB; AAT16470.  
 XX  
 PT Ligand for the hepatoma trans-membrane kinase receptor - useful for  
 PT stimulating and inhibiting cells carrying the receptor, e.g. for treating  
 PT neuro-degenerative disease.  
 XX  
 PS Claim 5; Fig 1(A-D); 88pp; English.  
 XX  
 CC Mouse (AAT16470) and human (AAT16471) Htk ligand which bind to, and  
 CC activate, the Htk receptor, have been identified in a variety of tissues  
 CC using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the  
 CC murine Htk ligand protein following a signal peptide cleavage is 34 kD  
 CC with an estimated pI of 8.9. The murine and human ligands show 96%  
 CC homology at the amino acid level. The DNA is used to produce recombinant  
 CC ligands; for tissue- specific typing (partic. as a marker for breast  
 CC cancer) and as a marker for human chromosome 13. The ligands (partic. in  
 CC soluble form) are used to activate the tyrosine kinase domain of the Htk  
 CC receptor, i.e. to stimulate or inhibit growth, differentiation, and/or  
 CC activation of cells contg. the receptor, e.g. treatment of  
 CC neurodegenerative diseases, since they are strongly expressed in the  
 CC cerebral cortex, hippocampus, striatum and cerebellum. The ligands are  
 CC also useful as a control or standard in assays, for generation of  
 CC antibodies, as a mol. wt. marker, for growth in vitro of Htk-receptor  
 CC positive cells, as research agent, in screening, etc  
 XX  
 SQ Sequence 336 AA;

Query Match 25.7%; Score 628.5; DB 2; Length 336;  
 Best Local Similarity 41.8%; Pred. No. 2.4e-44;  
 Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWN SANKRFQAE GGYVLYPQIGDRLDLLCPRARPPGPHSS 73  
 | |::| : : |||:||||:| :| | |||||:|:::|: :  
 Db 17 GLLMVL CRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73



PT and an Ephrin ligand, useful for promoting neovascularization, comprises  
PT contacting a Tie receptor with an Ephrin in the presence of a putative  
PT modulator.

XX

PS Example 1; Page 113-114; 199pp; English.

XX

CC The invention describes a method of identifying a modulator of binding  
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method  
CC comprises contacting a Tie receptor composition with an Ephrin  
CC composition in the presence and in the absence of a putative modulator  
CC compound, and detecting the binding between Tie receptor and the Ephrin  
CC in the presence and in the absence of the putative modulator. The method  
CC is useful for identifying a modulator of binding between a Tie receptor  
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the  
CC method are useful in modulating angiogenic processes, including  
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-  
CC Tie biology, aberrant growth, migration or proliferation of cells that  
CC express a Tie receptor, or for promoting growth of vessel or  
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or  
CC chronic compound, or a tissue graft or transplant). This is the amino  
CC acid sequence of mouse Ephrin-B2, a member of the Ephrin-B subclass of  
CC ligands that are bound to the membrane via a transmembrane domain and  
CC short cytoplasmic tail and function as Eph receptor ligands

XX

SQ Sequence 336 AA;

Query Match 25.6%; Score 626.5; DB 6; Length 336;  
Best Local Similarity 41.4%; Pred. No. 3.6e-44;  
Matches 137; Conservative 49; Mismatches 126; Indels 19; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWN SANKRFQ AEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73  
| |::| : : ||:||||:| :| | |||||:|::|: :  
Db 17 GLLMVL CRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy 74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133  
|:|:|:| | | | | | | | | | | | | | | | | :  
Db 74 GQYEYK VYVMVDKQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy 134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ-----SPRGGAVPRKPVSEMPME 187  
| | | | : | : | : | : | | | | | | | | | | : | |  
Db 134 DYYIIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNHGPTRRPELE---A 190

Qy 188 RDRGAHSL EPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGG 247  
| : : | : | | : : : | : : | | | : : :  
Db 191 GTNGRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVV 250

Qy 248 AMCWRRRRRAKPSERHPGPGSFGRGSLGLGGGGMGPREAEPGELGIALRGGAADPPF 307  
: | | : : | : | : | : | : | : | | |  
Db 251 LLLKYRRRHRKHSPQHTTTLSLSTLATPKRGNN---NGSEPSDVIIPLR---TADSVF 303

Qy 308 CPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY 338  
| | | | | | | | | | | : | | | | | |  
Db 304 CPHYEKVSGDYGHPVYIVQEMPPQSPANIIY 334

RESULT 12  
AAR55059

ID AAR55059 standard; protein; 346 AA.  
 XX  
 AC AAR55059;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-JAN-1995 (first entry)  
 XX  
 DE Elk tyrosine kinase receptor ligand.  
 XX  
 KW Vectors; elk-L protein; elk; ligands; cell growth; differentiation.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1. .24  
 FT /note= "signal peptide"  
 FT Protein 25. .346  
 FT /note= "mature elk-L protein"  
 XX  
 PN WO9411384-A1.  
 XX  
 PD 26-MAY-1994.  
 XX  
 PF 15-NOV-1993; 93WO-US010955.  
 XX  
 PR 13-NOV-1992; 92US-00977693.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Lyman S, Beckmann MP, Baum PR;  
 XX  
 DR WPI; 1994-183415/22.  
 DR N-PSDB; AAQ65486.  
 XX  
 PT New DNA encoding ligand for elk tyrosine kinase receptor - also related  
 PT polypeptides, vectors, antibodies and probes, useful e.g. in studying  
 PT cell differentiation or growth.  
 XX  
 PS Claim 7; Page 30; 35pp; English.  
 XX  
 CC The sequence is that of the elk-L protein able to bind elk, a tyrosine  
 CC kinase receptor. The DNA may be incorporated into vectors which can used  
 CC to study the role of elk and its ligands in cell growth and  
 CC differentiation. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 346 AA;

Query Match 25.4%; Score 623; DB 2; Length 346;  
 Best Local Similarity 39.2%; Pred. No. 7.4e-44;  
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy 8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61  
 || :| |: |: : | :||| |:| |:| : | |:|:|:|:|:|:  
 Db 4 PGQRWLGKWL VAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63  
 Qy 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121  
 |||| | :|:|:|:| | | :|:|:|:|:|:|:|:|:|:|:|:|:|:

Db 64 CPRAEAGRP-----Y EYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118  
 Qy 122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181  
 || | ||: ||||| :||:|: ||||: :||| | | ||::: || | :  
 Db 119 PNYMGLEFKKHHDYITSTSNGLGLENREGGVCRTMTMKIIMKVGQDPNAVTPQLTT 178  
 Qy 182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236  
 | | | : : || || : | | ||: || :  
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGDSGKHETVNQEEKSGP-----GASGGSSGDPD 231  
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSERHPGPGSFGSGGSLGL 277  
 : | ||| : | : | : : | : |  
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALSL 282  
 Qy 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333  
 || | || : : | | : : ||||| ||||| : |||||  
 Db 283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339  
 Qy 334 PNIYY 338  
 ||||  
 Db 340 ANIYY 344

RESULT 13

AAR91930

ID AAR91930 standard; protein; 346 AA.

XX

AC AAR91930;

XX

DT 25-MAR-2003 (revised)

DT 11-DEC-1996 (first entry)

XX

DE Human cytokine elk-ligand (elk-L).

XX

KW Human; cytokine; elk-ligand; elk-L; tyrosine kinase receptor;

KW neurotrophic; neuroprotective; placenta; radiolabelled probe; treatment;

KW neural tissue; excito-toxicity; injury; disorder; neural culture reagent;

KW immunogenic fragment; antibody.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .24

FT /label= sig\_peptide

FT Peptide 25. .346

FT /label= mat\_peptide

XX

PN US5512457-A.

XX

PD 30-APR-1996.

XX

PF 15-MAR-1994; 94US-00213403.

XX

PR 13-NOV-1992; 92US-00977693.

XX

PA (IMMV ) IMMUNEX CORP.

XX



AAW19249  
ID AAW19249 standard; protein; 346 AA.  
XX  
AC AAW19249;  
XX  
DT 25-MAR-2003 (revised)  
DT 18-AUG-1997 (first entry)  
XX  
DE Human elk ligand protien.  
XX  
KW Human; elk; ligand; elk-L; cytokine; testing; measuring; purification;  
KW neuroprotection; treatment; diabetic; hereditary; nutritional;  
KW neuropathy; neurodegenerative disease; tissue culture.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .24  
FT /label= sig\_peptide  
FT Peptide 25. .346  
FT /label= mat\_peptide  
XX  
PN US5627267-A.  
XX  
PD 06-MAY-1997.  
XX  
PF 01-JUN-1995; 95US-00458077.  
XX  
PR 13-NOV-1992; 92US-00977693.  
PR 15-MAR-1994; 94US-00213403.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Beckmann MP, Lyman S, Baum PR;  
XX  
DR WPI; 1997-271366/24.  
DR N-PSDB; AAT69766.  
XX  
PT Human elk ligand protein - for diagnostic or therapeutic use, e.g. as  
PT neuro-protective agent.  
XX  
PS Claim 1; Col 29-32; 18pp; English.  
XX  
CC The present sequence is a human elk ligand (elk-L) protein, which binds  
CC elk, has a calculated molecular weight of 35180 and an isoelectric point  
CC of 9.006. Elk-L is a cytokine that can be used to test cells for elk  
CC expression, measure the biological activity of elk, purify elk by  
CC affinity chromatography and as a neuroprotective agent to treat diabetic,  
CC hereditary and nutritional neuropathies and neurodegenerative diseases.  
CC It may also be added to tissue cultures to prolong the life of neurons.  
CC The elk-L cDNA was isolated from a human placental cDNA library, and is  
CC present as a cDNA insert in the recombinant vector deposited in strain  
CC ATCC 69085. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 346 AA;

Query Match

25.4%; Score 623; DB 2; Length 346;



Best Local Similarity 39.2%; Pred. No. 7.4e-44;  
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

Qy      8 PGGVRVGALLLLGLVGLVSGL-----SLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL 61
      ||  :|  |:  |:  :  |  :|||  |:|  |  :|  :  |  |:|:|:|:|:|:|:
Db      4 PGQRWLKWLAMVWVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRDLRFTIKFQEYS 121
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     64 CPRAEAGRP-----YEEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      ||  |  ||:  |||  |  :||:|:  |||:  :|||  ||  ||:  ::|  |  |  :
Db    119 PNYMGLEFKKHHDYIITSTSNGLSLEGLNREGGVCRTMTKIIMKVGQDPNAVTPQLTT 178

Qy    182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGGLA---- 236
      |  |  |  :  :  ||  ||  :  |  |  |  |  |  |  |  |  |  |  |  |
Db    179 SRPSKEADNTVKMATQAPGSRGSLGDSGKHETVNQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSESRRHPGPSFGRGGS LGL 277
      :  |  |||  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLRKRHRKHTQQ-----RAAALSL 282

Qy    278 -----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      ||  |  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339

Qy    334 PNIIY 338
      |||
Db    340 ANIIY 344

```

# RESULT 15

AAW36055

ID AAW36055 standard; protein; 346 AA.

XX

AC AAW36055;

XX

DT 06-MAR-1998 (first entry)

XX

DE Human elk-L protein.

XX

KW Human; elk-L; cytokine; ligand; tyrosine kinase receptor; fusion protein;

KW extracellular domain; immunoglobulin; neurological disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .24

FT /note= "signal peptide"

FT Protein 25. .346

FT /note= "mature protein"

FT Domain 25. .237

FT /note= "extracellular domain; this region is used to

FT generate a fusion protein with the Fc portion of the

FT human immunoglobulin G1"

FT Modified-site 139. .141



Qy 122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181  
 || | ||: ||||| :||:|: ||||: :||| || ||::: ||| | :  
 Db 119 PNYMGLEFKKHHDYIITSTSNGLSLEGLNREGGVCRTMTKIIMKVGQDPNAVTPQLTT 178  
 Qy 182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236  
 | | | : : || || : | | ||: || :  
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231  
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277  
 : | || : | : | : : | : | |  
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ-----RAAALSL 282  
 Qy 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333  
 || | || : : || : : ||||| ||||| : |||||  
 Db 283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339  
 Qy 334 PNIYY 338  
 ||||  
 Db 340 ANIYY 344

Search completed: September 15, 2004, 12:35:56  
 Job time : 107.591 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:32:56 ; Search time 27.4717 Seconds  
(without alignments)  
855.055 Million cell updates/sec

Title: US-10-021-121-2  
Perfect score: 2450  
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8							
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
1	1837	75.0	340	4	US-09-214-631-3	Sequence 3, Appli	
2	1835	74.9	340	4	US-09-051-994-2	Sequence 2, Appli	
3	628.5	25.7	336	1	US-08-436-044-2	Sequence 2, Appli	
4	628.5	25.7	336	2	US-08-436-054-2	Sequence 2, Appli	
5	628.5	25.7	336	5	PCT-US95-08812-2	Sequence 2, Appli	
6	623	25.4	346	1	US-08-213-403-2	Sequence 2, Appli	
7	623	25.4	346	1	US-08-458-077-2	Sequence 2, Appli	
8	623	25.4	346	1	US-08-460-741-2	Sequence 2, Appli	
9	623	25.4	346	1	US-08-747-240-2	Sequence 2, Appli	
10	623	25.4	346	1	US-08-299-567-6	Sequence 6, Appli	
11	623	25.4	346	4	US-09-039-642B-2	Sequence 2, Appli	

; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-214-631-3

Query Match 75.0%; Score 1837; DB 4; Length 340;  
Best Local Similarity 99.7%; Pred. No. 4.3e-146;  
Matches 337; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60
          |||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
          |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLQVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300
          |||
Db    241 GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYY 338
          |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYY 338
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RESULT 2

US-09-051-994-2

; Sequence 2, Application US/09051994A  
; Patent No. 6602683  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS  
; FILE REFERENCE: REG-341-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/051,994A  
; CURRENT FILING DATE: 1998-04-24  
; EARLIER APPLICATION NUMBER: PCT/US96/17201  
; EARLIER FILING DATE: 1996-10-25  
; EARLIER APPLICATION NUMBER: 60/007,015  
; EARLIER FILING DATE: 1995-10-25  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Homo sapiens



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; FEATURE:
; NAME/KEY: site
; LOCATION: (166)
; OTHER INFORMATION: Xaa=Arg or Gln
US-09-051-994-2
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Query Match          74.9%; Score 1835; DB 4; Length 340;
Best Local Similarity 99.7%; Pred. No. 6.4e-146;
Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL 60
          |||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLDLRFTIKFQ EY 120
          |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLDLRFTIKFQ EY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPS ESRHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300
          |||
Db    241 GVAGAGGAMCWRRRRRAKPS ESRHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQ SPPNIYY 338
          |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQ SPPNIYY 338
```

# RESULT 3

US-08-436-044-2

```
; Sequence 2, Application US/08436044
; Patent No. 5624899
```

## ; GENERAL INFORMATION:

```
; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
```

## ; CORRESPONDENCE ADDRESS:

```
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
```

## ; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
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## ; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/436,044
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-436-044-2

```

```

Query Match          25.7%; Score 628.5; DB 1; Length 336;
Best Local Similarity 41.8%; Pred. No. 8.2e-45;
Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

```

```

Qy      14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | | | | | | | | | | | : :
Db      17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy      74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
      ||:|:|:|:| | | | | | | | | | | | | | | | | | : :
Db      74 GQYEYKVMVDKQDQADRCTIKKENTPLLCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy     134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      |||:|:|:|:| | | | : | | | | | | | | | | | | : |
Db     134 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy     191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : | | : : : | : : | | | | : : : : :
Db     194 GRSSTTSPFVKPNPGSSDTGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy     251 WRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
      ||| : : | : : | : | : | | : | : | | | | | | |
Db     254 KYRRRHRKHSPQH TTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

Qy     311 YEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
      ||| | | | | | | | | | | | | | | | | | | | | |
Db     307 YEKVSGDYGHPVYIVQEMPPQSPANIYY 334

```

```

RESULT 4
US-08-436-054-2
; Sequence 2, Application US/08436054
; Patent No. 5864020
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William

```



```

; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,054
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-436-054-2

```

```

Query Match          25.7%; Score 628.5; DB 2; Length 336;
Best Local Similarity 41.8%; Pred. No. 8.2e-45;
Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

```

```

Qy      14 GALLLLGLVGLVSGLSLEPVYWNNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||::|::|: :
Db      17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy      74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRLRFTIKFQEYSPNLWGHEFRSHH 133
      ||:|:|:| | | | || | || |::|:|||||:| || | ||:
Db      74 GQYEYKVMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy     134 DYYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      ||||:|:|:| |||:::| || | ||:|:| || | | | :|
Db     134 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy     191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | :: : | : || | : : : :
Db     194 GRSSTTSFVKPNPGSSDTGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy     251 WRRRRRAKPSESRHPGPGSFGRGSSLGLGGGGMGMPREAPGELGIALRGGGAADPPFCPH 310

```

```

      ||| : :| | : || :|| :: | || || |||
Db      254 KYRRRHRKHSPQHHTTSLSLSTLATPKRGGNN----NGSEPSDVIPLR---TADSVFCPH 306

Qy      311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
      |||||: |||| ||||
Db      307 YEKVSGDYGHPVYIVQEMPPQSPANIYY 334

```

RESULT 5

PCT-US95-08812-2

; Sequence 2, Application PC/TUS9508812

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; TITLE OF INVENTION: HTK LIGAND

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08812

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 00,000

; REFERENCE/DOCKET NUMBER: 902PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 336 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

PCT-US95-08812-2

Query Match 25.7%; Score 628.5; DB 5; Length 336;

Best Local Similarity 41.8%; Pred. No. 8.2e-45;

Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

```

Qy      14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::|: :
Db      17 GLLMVLCRTAISRSIVLEPIYWSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

```

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; Sequence 2, Application US/08213403
; Patent No. 5512457
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5512457el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,403
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430

```

; TELEFAX: (206) 233-0644  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 346 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-213-403-2

Query Match 25.4%; Score 623; DB 1; Length 346;  
 Best Local Similarity 39.2%; Pred. No. 2.5e-44;  
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy	8	PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL	61
		:   :  : :   :     :   :  :   : : : : :	
Db	4	PGQRWLKGWLVMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII	63
Qy	62	CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS	121
		: : : :      : : : : :  : : : : :	
Db	64	CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS	118
Qy	122	PNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV	181
		: : : : : : : : : : : : : : : : :	
Db	119	PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTMTMKIIMKVGQDPNAVTPPEQLTT	178
Qy	182	SEMPMERDRGAAHSLE-PGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLA----	236
		: :       :       : :  :	
Db	179	SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVQNQEEKSGP-----GASGGSSGDPD	231
Qy	237	-----LLLLGVAGAGGA-----MCWRRRRRAKPSESRRHPGPGSFGRGGSGLGL	277
		:       :  :   :  :  :	
Db	232	GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLLKLRKRHRKHTQQ-----RAAALSL	282
Qy	278	----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP	333
		:     : : : : : : : : : : : :	
Db	283	STLASPKGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP	339
Qy	334	PNIIY 338	
Db	340	ANIIY 344	

# RESULT 7

US-08-458-077-2

; Sequence 2, Application US/08458077  
 ; Patent No. 5627267

## ; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.  
 ; APPLICANT: Beckmann, M. Patricia  
 ; APPLICANT: Baum, Peter R  
 ; APPLICANT: Carpenter, Melissa  
 ; TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle

```

; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,077
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-077-2

```

```

Query Match          25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 2.5e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

```

Qy      8 PGGVRV GALLLLGVLGLVSGL-----SLEPVYWN SANKRFQAEGGYVLYPQIGDRLDLL 61
      ||  :| |: |: : | :||| |:| |:| : | :|:|:|:|:|:|
Db      4 PGQRWL GKWL VAMV V WALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQEYS 121
      ||| | | :|:|:| | | | | :|:|:|:|:| :|:|:|:|:|
Db     64 CPRAEAGRP-----YEYKLYLV RPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIITATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      || | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    119 PNYMGLEFKKHHDYIITSTNGSLEGL ENREGGVCRTRTMKIIMKVGQDPNAVTP EQLT 178

Qy    182 SEMP MERDRGA AHSLE-PGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      | | | : : || | | : | | | :|:|:|
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      : | || | : |:| |:| : | :| |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLL LKLRK RHRKHTQQ-----RAAALSL 282

```

Qy 278 ----GGGGMGMPREAEPEGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333  
 || | || :: | || : : ||||| ||||| : |||||  
 Db 283 STLASPKGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339  
 Qy 334 PNIYY 338  
 ||||  
 Db 340 ANIYY 344

RESULT 8

US-08-460-741-2

; Sequence 2, Application US/08460741

; Patent No. 5670625

; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; APPLICANT: Beckmann, M. Patricia

; APPLICANT: Baum, Peter R

; APPLICANT: Carpenter, Melissa

; TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple System 7.1

; SOFTWARE: Microsoft Word for Apple, Version 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/460,741

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/213,403

; FILING DATE: 15-MAR-1994

; APPLICATION NUMBER: US 07/977,693

; FILING DATE: 13-NOV-1992

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Seese, Kathryn A.

; REGISTRATION NUMBER: 32,172

; REFERENCE/DOCKET NUMBER: 2807-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 346 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-460-741-2

Query Match 25.4%; Score 623; DB 1; Length 346;  
 Best Local Similarity 39.2%; Pred. No. 2.5e-44;  
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

Qy      8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLL 61
      ||  :| |: |: : |      :||| |:| |:| : | |:|:|:|:|:|:|
Db      4 PGQRWLKGWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
      |||| |      ||:||||| | |      ||:|:|:|:|:|:|:|:|:|
Db     64 CPRAEAGRP-----YEEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      || | ||: ||||| :|:|: | |||: :||| | | ||:::| | |      :
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQLTT 178

Qy    182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      |  | |      : : ||      ||      : | |      ||:| | :
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDSGKHETV NQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      : |      |||      : |:| | :|      | :| |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALSL 282

Qy    278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      || | || :| | |      : : |||||:|:|:|:|:|:|:|:|:|
Db    283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339

Qy    334 PNIIY 338
      ||||
Db    340 ANIIY 344
  
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# RESULT 9

US-08-747-240-2

; Sequence 2, Application US/08747240

; Patent No. 5728813

; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; APPLICANT: Beckmann, M. Patricia

; APPLICANT: Baum, Peter R

; APPLICANT: Carpenter, Melissa

; TITLE OF INVENTION: No. 5728813el Cytokine Designated elk Ligand

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple System 7.1

; SOFTWARE: Microsoft Word for Apple, Version 5.1a

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/747,240
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-747-240-2

```

```

Query Match          25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 2.5e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

```

Qy      8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL 61
      ||  :|  |:  |:  :  |  :|||  |:|  |:|  :  |  |:|:|:|:|:|:|:
Db      4 PGQRWLKGKWLAMVWVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPLDLRFTIKFQEYS 121
      |||  |  :  :|:|:|:|  |  |  :|:|:|:|:|:  :|:|:|:|:|:|
Db     64 CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
      ||  |  |:  |||:|  :|:|:|  |||:  :|:|  ||  |:|:|:|  |  :
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQLTT 178

Qy    182 SEMPMERDRGAHSLPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      |  |  |  :  :  ||  ||  :  |  |  |  :|:|  :
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSESRRHPGPGSFGRGGSGLGL 277
      :  |  |||  :  :|  |  :  :  |  :|  |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLLKLRKRHRKHTQQ-----RAAALSL 282

Qy    278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      ||  |  ||  :  :  ||  :  :|:|:|:|:|:|:|:|:|:|:|:|:|
Db    283 STLASPKGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339

Qy    334 PNIYY 338
      |||
Db    340 ANIYY 344

```



RESULT 10  
 US-08-299-567-6  
 ; Sequence 6, Application US/08299567  
 ; Patent No. 5747033  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis, et al.  
 ; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL  
 ; TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 ; STREET: 777 Old Saw Mill River Road  
 ; CITY: Tarrytown  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10591-6707  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/299,567  
 ; FILING DATE: 01-SEP-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kempner, Gail M.  
 ; REGISTRATION NUMBER: 32,143  
 ; REFERENCE/DOCKET NUMBER: REG 290  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 914-345-7400  
 ; TELEFAX: 914-345-7721  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 346 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 US-08-299-567-6

Query Match 25.4%; Score 623; DB 1; Length 346;  
 Best Local Similarity 39.2%; Pred. No. 2.5e-44;  
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY	8	PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL	61
		:   :  : :   :     :   :  :    : : : : : :	
Db	4	PGQRWLKGKWLVMVWALCRLATPLAKNLEPVSWSSSLNPKFLSGKGLVIYPKIGDKLDII	63
QY	62	CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRPLDLRFTIKFQEYS	121
		: : : :        : : : : : : : : : : :	
Db	64	CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS	118
QY	122	PNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV	181
		: : : : : : : : : : : : : : : : : :	
Db	119	PNYMGLEFKKHHDYIITSTNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPPEQLTT	178

Qy 182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236  
 | | | : : | | : | | : : :  
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231  
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSERHPGPGSFGRGGS LGL 277  
 : | | | : | : | : : | : |  
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALSL 282  
 Qy 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333  
 | | | | : : | | : : | | | | | | | | | | | | | | | |  
 Db 283 STLASPKGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339  
 Qy 334 PNIYY 338  
 | | | |  
 Db 340 ANIYY 344

RESULT 11

US-09-039-642B-2

; Sequence 2, Application US/09039642B

; Patent No. 6540992

; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; APPLICANT: Beckmann, M. Patricia

; APPLICANT: Baum, Peter R.

; APPLICANT: Carpenter, Melissa K.

; TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND

; FILE REFERENCE: GENENT.67CPDV3

; CURRENT APPLICATION NUMBER: US/09/039,642B

; CURRENT FILING DATE: 1998-03-16

; PRIOR APPLICATION NUMBER: 08/213,403

; PRIOR FILING DATE: 1994-03-15

; PRIOR APPLICATION NUMBER: 07/977,693

; PRIOR FILING DATE: 1992-11-13

; PRIOR APPLICATION NUMBER: 08/747,240

; PRIOR FILING DATE: 1996-10-12

; PRIOR APPLICATION NUMBER: 08/460,741

; PRIOR FILING DATE: 1995-06-02

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 346

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-039-642B-2

Query Match 25.4%; Score 623; DB 4; Length 346;

Best Local Similarity 39.2%; Pred. No. 2.5e-44;

Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy 8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 61  
 | | : | : : : | : | | : | : | : | : | : | : | : | : | :  
 Db 4 PGQRWLKGWLVAMVWALCRLATPLAKNLEPVSWSSSLNPKFLSGKGLVIYPKIGDKLDII 63  
 Qy 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQEYS 121  
 | | | | | : | | | | | : | | : : | : | : : | : | : | : | : | : | :  
 Db 64 CPRAEAGRP-----Y EYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIREFTIKFQEFS 118

Qy 122 PNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181  
 || | ||: ||||| :||:|: ||||: :||| || ||:::|||| | :  
 Db 119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQLTT 178  
 Qy 182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236  
 | | | : : || | | : | | | ||:| | :  
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231  
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSERHPGPGSFGRGGSGLGL 277  
 : | || | : | | | : : | : |  
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLRKRRKHTQQ-----RAAALSL 282  
 Qy 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333  
 || | || : : | | : : ||||| ||||| : |||||  
 Db 283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339  
 Qy 334 PNIYY 338  
 ||||  
 Db 340 ANIYY 344

RESULT 12

US-08-436-044-4

; Sequence 4, Application US/08436044

; Patent No. 5624899

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.

; APPLICANT: Matthews, William

; TITLE OF INVENTION: HTK LIGAND

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/436,044

; FILING DATE: 05-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/277722

; FILING DATE: 20-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 00,000

; REFERENCE/DOCKET NUMBER: 902D3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 333 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 US-08-436-044-4

Query Match 25.3%; Score 620.5; DB 1; Length 333;  
 Best Local Similarity 40.5%; Pred. No. 3.8e-44;  
 Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

Qy 14 GALLLLGLVGLVSGLSLEPVYWN SANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73  
 | |::| : : |||:||||:| :| | |||||:|::|: :  
 Db 14 GVLMLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70  
 Qy 74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLTCDRDLRLRFTIKFQEYSPNLWGHEFRSHH 133  
 ||::|:| | || || | :| |::| |||||:| |||| |:: :  
 Db 71 GQY EYKVMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130  
 Qy 134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190  
 ||||:|:|: |||:: :||| || |:::| | | : | :|  
 Db 131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190  
 Qy 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250  
 | : : | : || | : : : : || | : : : :  
 Db 191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250  
 Qy 251 WRRRRRAKPSESRHPGPGSFGRRGSLGLGGGGMGPREAEPGELGIALRGGAADPPFCPH 310  
 ||| : :| | : | :|| : : | || || ||||  
 Db 251 KYRRHRHRKHSPQHTTTLSTLATPKRSGNN---NGSEPSDIIIPLR---TADSVFCPH 303  
 Qy 311 YEKVSGDYGHPVYIVQDGPPQSPNIIY 338  
 |||||: |||| ||||  
 Db 304 YEKVSGDYGHPVYIVQEMPPQSPANIY 331

# RESULT 13

US-08-436-054-4

; Sequence 4, Application US/08436054  
 ; Patent No. 5864020

## ; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.  
 ; APPLICANT: Matthews, William  
 ; TITLE OF INVENTION: HTK LIGAND  
 ; NUMBER OF SEQUENCES: 7

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

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;   SOFTWARE:  patin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/436,054
;     FILING DATE:  05-MAY-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/277722
;     FILING DATE:  20-JUL-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Lee, Wendy M.
;     REGISTRATION NUMBER:  00,000
;     REFERENCE/DOCKET NUMBER:  902D1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415/225-1994
;     TELEFAX:  415/952-9881
;     TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  333 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-436-054-4

```

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Query Match          25.3%;  Score 620.5;  DB 2;  Length 333;
Best Local Similarity 40.5%;  Pred. No. 3.8e-44;
Matches 133;  Conservative 52;  Mismatches 130;  Indels 13;  Gaps 5;

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Qy      14 GALLLLGLVGLVSGLSLEPVYWNANKRFQAEAGGYVLYPQIGDRDL DLCPRARPPGPHSS 73
      | |::|   :   : |||:||||:| :|   | |||||::|::|::|   :
Db      14 GVLMLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy      74 PNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFITIKFQEYSPNLWGHEFRSHH 133
      ||::|::|:|   |   ||   || | :|| |::| |||||::| ||||| |::| :
Db      71 GQYEYYKVYMDKDKQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy     134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      |||||::|::|:| |||:: :||| || ||::|::| || |   : |   :|
Db     131 DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy     191 GAAHSLEPGKENLPGDPTSNAISRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : | | | : : : : : : : | | | : : : :
Db     191 GRSSTTSPFVKPNPGSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy     251 WRRRRRAKPSESRHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGGAADPPFCPH 310
      ||| :   :|   |   :   |   :|| : : | ||   || |||
Db     251 KYRRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy     311 YEKVSGDYGHPVYIVQDGPPQSPNNIYY 338
      ||||| ||||| ||||| : |||| ||||
Db     304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331

```

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RESULT 14
US-08-271-948-2
; Sequence 2, Application US/08271948
; Patent No. 6303769
; GENERAL INFORMATION:

```

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; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Reddy, Pranhitha
; TITLE OF INVENTION: No. 6303769e1 Cytokine Designated Lerk-5
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,948
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2823
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-271-948-2

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Query Match          25.3%; Score 620.5; DB 4; Length 333;
Best Local Similarity 40.5%; Pred. No. 3.8e-44;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

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Qy      14 GALLLLGVLGLVSGLSLEPVYWNANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : ||::|||::| :| | |||||::|::|::| :
Db      14 GVLMLVCRTAISKIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy      74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRPDLDRFTIKFQEYSPNLWGHEFRSHH 133
      ||::|::| | || || | :|| |::|||::|::|::| |::| :
Db      71 GQYEYYKVMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy     134 DYYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      |||::|::|::| |::| :||| || ||::|::| | | : | :|
Db     131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy     191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | :: : : : : || | | : :: : :
Db     191 GRSSTTSPFVKPNPGSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy     251 WRRRRRAKPSESRRHPGPSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310

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Db 251 KYRRHRKHSPQHHTTTLSTLATPKRSGNN---NGSEPSDIIPLR---TADSVFCPH 303  
 QY 311 YEKVSGDYGHPVYIVQDGPPQSPNIIY 338  
 Db 304 YEKVSGDYGHPVYIVQEMPPQSPANIIY 331

RESULT 15

US-08-739-333-2

; Sequence 2, Application US/08739333

; Patent No. 6479459

; GENERAL INFORMATION:

; APPLICANT: Cerretti, Douglas P.

; APPLICANT: Reddy, Pranhitha

; TITLE OF INVENTION: No. 6479459el Cytokine Designated Lerk-5

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple 7.1

; SOFTWARE: Microsoft Word, Version 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/739,333

; FILING DATE: 29-OCT-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/271,948

; FILING DATE: 08-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Seese, Kathryn A.

; REGISTRATION NUMBER: 32,172

; REFERENCE/DOCKET NUMBER: 2823

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644

; TELEX: 756822

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 333 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-739-333-2

Query Match 25.3%; Score 620.5; DB 4; Length 333;

Best Local Similarity 40.5%; Pred. No. 3.8e-44;

Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

QY 14 GALLLLGVLGLVSGLSLEPVYWSANKRFQAEAGGYVLYPQIGDRDLLCPRARPPGPHSS 73

Db	14	GVLMLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV	70
Qy	74	PNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEYSPNLWGHEFRSHH	133
Db	71	GQYEEYKVMVDKDQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK	130
Qy	134	DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR	190
Db	131	DYYIIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN	190
Qy	191	GAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC	250
Db	191	GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL	250
Qy	251	WRRRRAKPSESRRHPGPGSFGRGGSGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH	310
Db	251	KYRRRRHRKHSPQHTTTLSLSTLATPKRSGNN---NGSEPSDIIIPLR---TADSVFCPH	303
Qy	311	YEKVS GDYGHFVYIVQDGPPQSPPNIYY	338
Db	304	YEKVS GDYGHFVYIVQEMPPQSPANIYY	331

Search completed: September 15, 2004, 12:41:03  
Job time : 29.4717 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:30:30 ; Search time 29.761 Seconds  
 (without alignments)  
 1470.620 Million cell updates/sec

Title: US-10-021-121-2  
 Perfect score: 2450  
 Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_78:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	628.5	25.7	336	2 I49766	hepatoma transmemb
2	623	25.4	346	2 S46993	elk ligand - human
3	620.5	25.3	333	2 I84743	hepatoma transmemb
4	604.5	24.7	345	2 I48780	Stral/Eplg2 protei
5	599.5	24.5	345	2 I58406	LERK-2 - rat
6	214.5	8.8	237	2 T19914	hypothetical prote
7	179	7.3	238	2 I38849	LERK-3 - human
8	176	7.2	209	2 A54984	ELF-1 protein prec
9	175.5	7.2	213	2 JE0322	ephrin-A2 - human
10	170.5	7.0	228	2 A57084	repulsive axon gui
11	169.5	6.9	201	2 I38850	LERK-4 - human
12	167.5	6.8	228	2 I58170	LERK-7 precursor -
13	166	6.8	205	2 A36377	B61 protein precur

14	159	6.5	680	2	S31216	collagen alpha 1(X
15	154.5	6.3	1049	1	CGBO7S	collagen alpha 1(I
16	153.5	6.3	1670	1	CGHU3B	collagen alpha 3(I
17	151.5	6.2	301	2	B31219	collagen 2 - Caeno
18	149	6.1	325	2	T32248	hypothetical prote
19	149	6.1	569	2	S42886	collagen - silkwor
20	148.5	6.1	316	2	T20497	hypothetical prote
21	148	6.0	921	2	S42617	collagen alpha 1(I
22	146.5	6.0	1315	2	A56101	collagen alpha 1(X
23	146.5	6.0	1492	2	A40333	collagen alpha 1'(
24	146.5	6.0	1774	2	B56101	collagen alpha 1(X
25	146	6.0	675	2	S20819	collagen alpha 3(I
26	145.5	5.9	305	2	T20906	hypothetical prote
27	145	5.9	674	2	S13301	collagen alpha 1(X
28	145	5.9	931	2	S13580	collagen alpha 1(I
29	144.5	5.9	438	2	S53787	collagen alpha cha
30	144	5.9	1027	2	S28774	collagen alpha cha
31	143	5.8	1747	2	A54121	collagen alpha-4 c
32	142.5	5.8	635	2	A57131	collagen alpha 2(V
33	142.5	5.8	743	1	S23779	collagen alpha 1(V
34	142.5	5.8	1496	1	CGHU2V	collagen alpha 2(V
35	142	5.8	614	2	T33149	hypothetical prote
36	142	5.8	744	2	S15435	collagen alpha 1(V
37	142	5.8	1029	1	S21369	collagen alpha 2(V
38	142	5.8	1763	2	S16366	collagen alpha 2(I
39	141.5	5.8	1466	1	CGHU7L	collagen alpha 1(I
40	141	5.8	319	2	T32250	hypothetical prote
41	141	5.8	744	1	A34246	collagen alpha 1(V
42	141	5.8	744	1	S23298	collagen alpha 1(V
43	140.5	5.7	305	2	T30165	hypothetical prote
44	140	5.7	304	2	T22482	hypothetical prote
45	140	5.7	680	1	CGHU1D	collagen alpha 1(X

#### ALIGNMENTS

##### RESULT 1

I49766

hepatoma transmembrane kinase ligand - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I49766

R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews, W.

Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995

A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kinase Htk.

A;Reference number: I49766; MUID:95199254; PMID:7534404

A;Accession: I49766

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-336 <RES>

A;Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678

C;Genetics:

A;Gene: HTK



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Db      64 CPRAEAGRP-----Y EYYKLYLVLRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
QY      122 PNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
Db      119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTMTMKIIMKVGQDPNAVTPQLTT 178
QY      182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
Db      179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
QY      237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSERHPGPGSFGRGGS LGL 277
Db      232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLRKHRKHTQQ-----RAAALSL 282
QY      278 ----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
Db      283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
QY      334 PNIYY 338
Db      340 ANIYY 344

```

# RESULT 3

I84743

hepatoma transmembrane kinase ligand - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 05-Nov-1999

C;Accession: I84743

R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews, W.

Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995

A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kinase Htk.

A;Reference number: I49766; MUID:95199254; PMID:7534404

A;Accession: I84743

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-333 <RES>

A;Cross-references: GB:L38734; NID:g769675; PIDN:AAC41752.1; PID:g769676

C;Genetics:

A;Gene: GDB:EPLG5; LERK5

A;Cross-references: GDB:438338; OMIM:600527

A;Map position: 13q33-13q33

Query Match 25.3%; Score 620.5; DB 2; Length 333;

Best Local Similarity 40.5%; Pred. No. 1e-36;

Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

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QY      14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDLLCPRARPPGPHSS 73
Db      14 GVLMVLCRTAISKSIVLEPIYWNSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
QY      74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLRFTIKFQEYSPNLWGHEFRSHH 133
Db      71 GQY EYYKVYMDKQDQADRCTIKKENTPLLCAKPDQDIKFTIKFQEFS PNLWGLEFQKNK 130

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QY 134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190  
 ||||:|:|:|: |||: :||| || ||:|:| || | : | :|  
 Db 131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190  
 QY 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250  
 | : : | : || | : : : : || | : : : :  
 Db 191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250  
 QY 251 WRRRRRAKPSESRHPGPGSFGRGGSLLGLGGGGMGMPREAEPEGELGIALRGGGAADPPFCPH 310  
 ||| : :| | : | :|| :| || || || ||  
 Db 251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN---NGSEPSDIIPLR---TADSVFCPH 303  
 QY 311 YEKVSGDYGHPVYIVQDGPPQSPNIIY 338  
 ||||| ||||| ||||| : |||| ||||  
 Db 304 YEKVSGDYGHPVYIVQEMPPQSPANIIY 331

#### RESULT 4

I48780

Stral/Eplg2 protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I48780; A55507; A55062; S52670

R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Dolle, P.; Chambon, P.

Dev. Biol. 170, 420-433, 1995

A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryonal carcinoma cells and characterization of a novel mouse gene, Stral (mouse LERK-2/Eplg2).

A;Reference number: I48780; MUID:95377533; PMID:7649373

A;Accession: I48780

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-345 <RES>

A;Cross-references: EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859

R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Davison, B.L.

Genomics 24, 127-132, 1994

A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene encoding a binding protein for the receptor tyrosine kinase Elk.

A;Reference number: A55507; MUID:95203867; PMID:7896266

A;Accession: A55507

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-345 <FLE>

A;Cross-references: GB:U07598

R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.  
 J. Biol. Chem. 269, 26606-26609, 1994

A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyrosine kinase.

A;Reference number: A55062; MUID:95014510; PMID:7929389

A;Accession: A55062

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-89, 'T', 91-345 <SHA>

A;Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929

C;Genetics:  
A;Gene: EPLG2

Query Match 24.7%; Score 604.5; DB 2; Length 345;  
Best Local Similarity 37.9%; Pred. No. 1.5e-35;  
Matches 136; Conservative 51; Mismatches 107; Indels 65; Gaps 10;

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QY      15 ALLLLGVLGLVSG--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS 72
      |:::| : | : | : ||| | : | : | : | : ||: ||: ||: ||: |
Db      15 AMVVLTLCLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72

QY      73 SPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRDLDRFTIKFQEYSPNLWGHEFRSH 132
      ||: ||||| | | | | : | : | : | : ||: ||| | ||: :
Db      73 ---YEYYKLYLVRPEQAAACSTVLDPNVLTCKNPKHQEIRFTIKFQEYSPNYMGLEFKKY 129

QY     133 HDYIIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGA 192
      ||||| : ||: | : ||| : : ||| | | ||: : ||| | | : : | :
Db     130 HDYYITSTSNGLSLEGLNREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188

QY     193 AHSLEPGKENLPGDPTSNATSRGAEGP-----LPPPSMPAVAGAAGG-----LA 236
      : : | ||: | | | | |
Db     189 VKT-----ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGDSDSFFNSK 236

QY     237 LLLLG VAGAGGA-----MCWRRRRRAKPSESRHPGPGSFGRGGS LGL----GG 279
      : | ||| : | : | : | : | : |
Db     237 VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ-----RAAALSSTLASP 287

QY     280 GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
      || | || : : | | : : ||| ||| ||| ||| : ||| |||
Db     288 KGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 343
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RESULT 5

I58406

LERK-2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I58406

R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollingsworth, T.; VandenBos, T.; Davison, B.L.; Lyman, S.D.; Beckmann, M.P. Oncogene 9, 3241-3248, 1994

A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conserved and expressed in a developmentally regulated pattern.

A;Reference number: I58406; MUID:95022634; PMID:7936648

A;Accession: I58406

A;Status: preliminary; translated from GB/EMBL/EDBJ

A;Molecule type: mRNA

A;Residues: 1-345 <RES>

A;Cross-references: EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119

C;Genetics:

A;Gene: Eplg2

Query Match 24.5%; Score 599.5; DB 2; Length 345;  
Best Local Similarity 37.6%; Pred. No. 3.3e-35;  
Matches 135; Conservative 52; Mismatches 107; Indels 65; Gaps 10;

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QY      15 ALLLLGVLGLVSG--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS 72
```

```

      |::| : | : | :||| :| | : | :|::|::|::|::|::|
Db      15 AMVVLTLCLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72
QY      73 SPNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRLRFTIKFQEYSPNLWGHEFRSH 132
      ||:||||| | | |::|::|::|::|::|::|::|::|::|::|
Db      73 ---YEYKLYLVLRPEQAAACSTVLDPNVLVTCNKPQQEIRFTIKFQEFSFNYMGLEFKKY 129
QY      133 HDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPKRPVSEMPMERDRGA 192
      |||| :|::| :||| :||| || |:::| | | : : | :
Db      130 HDYIITSTSNGLSLEGLNREGGVCRTMTKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188
QY      193 AHSLEPGKENLPGDPTSNATSRGAEGP-----LPPPSMPAVAGAAGG-----LA 236
      : : | |::| | | | : |
Db      189 VKT-----ATQAPGRGSQGSDGKHETVNQQEKGSGPGAGSGSGDTSFFNSK 236
QY      237 LLLLGAVAGAGGA-----MCWRRRRRAKPSERHPGPGSFGRGGSGLGL----GG 279
      : | || | : | | : : | : |
Db      237 VALFAAVGAGCVIFLLIIIFLTVLLLLKLRKRHRKHTQQ-----RAAALSLSLTLASP 287
QY      280 GGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNIIYY 338
      | | || :| | | : :|::|::|::|::|::|::|::|::|
Db      288 KGDSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIIYY 343

```

RESULT 6

T19914

hypothetical protein C43F9.8 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T19914

R;Mortimore, B.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19195

A;Accession: T19914

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-237 <WIL>

A;Cross-references: EMBL:Z82262; PIDN:CAB54195.1; GSPDB:GN00022; CESP:C43F9.8

A;Experimental source: clone C43F9

C;Genetics:

A;Gene: CESP:C43F9.8

A;Map position: 4

A;Introns: 32/2; 96/3; 214/1

Query Match 8.8%; Score 214.5; DB 2; Length 237;

Best Local Similarity 25.7%; Pred. No. 3.9e-08;

Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps 6;

```

QY      11 VRVGALLLLGLVGLVS-GLSLEPVYWNANKRFQAEG-GYVLYPQIGDRDLDCPRARPP 68
      :: :| : : : : | | | : | : ||| : |::
Db      1 MQIATFILLSLFPFIGWARKIPDINWISSNPIFDVSNTHVISVHIGDRVSIRCPKSDET 60
QY      69 GPHSSPNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRLRFTIKFQEYSPNLWGHE 128
      | ||: :| : | | | : || : : | : :| | |
Db      61 G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE 114
QY      129 FRSHHDYIIA-----TSDGTREGLESQGGVCLTRGMKVLLRVGQ 169

```

```

      |:  :|::|:  ||||| ||::  : |:|  : ||:  |||
Db      115 FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKKDGLCTAKQMKIKFEVGQ 174
QY      170 SPRGGAVPRKPVSEMPMERDRGAAHS 195
      ||  |:  :  ::||| ||
Db      175 DRRGIENPK--FAARTLKKDRDAEHS 198

```

RESULT 7

I38849

LERK-3 - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 29-Sep-1999

C;Accession: I38849

R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.;  
Lyman, S.D.; Srinivasan, S.; Fletcher, F.A.; Gayle, R.B.  
Oncogene 10, 299-306, 1995

A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of  
cDNAs encoding a family of proteins.

A;Reference number: I38849; MUID:95140419; PMID:7838529

A;Accession: I38849

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-238 <RES>

A;Cross-references: EMBL:U14187; NID:g642832; PIDN:AAC50078.1; PID:g642833

C;Genetics:

A;Gene: GDB:EPLG3

A;Cross-references: GDB:438336; OMIM:601381

A;Map position: 1q21-1q22

C;Superfamily: axon guidance signal protein

```

Query Match          7.3%;  Score 179;  DB 2;  Length 238;
Best Local Similarity 28.4%;  Pred. No. 1.3e-05;
Matches 65;  Conservative 24;  Mismatches 80;  Indels 60;  Gaps 12;

```

```

QY      7  GPGGVVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R 64
      |||  -----| ||  :  |||||:::  : | ||  :  | ||: ||
Db      24  GPG-----GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67

QY      65  ARPPGPHSSP----NYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDR PDL---DLRFTIKF 117
      :  || : |  | | ||:|  | | |  | :||  :||: ||
Db      68  SSGVGPAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126

QY      118  QEYSPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVP 177
      | ||  |::| : |::| |:|  ||  ||| :  :  |
Db      127  QRISAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG--- 174

QY      178  RKPVSEMP-----MERDRGAAHSLE-----PGKENLP 204
      ||| :|  | :  ||  | :|||
Db      175  EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223

```

RESULT 8

A54984

ELF-1 protein precursor - mouse

N;Alternate names: Cek7 ligand

C;Species: Mus musculus (house mouse)



C;Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 29-Sep-1999  
 C;Accession: A54984; A55873  
 R;Cheng, H.J.; Flanagan, J.G.  
 Cell 79, 157-168, 1994  
 A;Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the Mek4 and Sek receptor tyrosine kinases.  
 A;Reference number: A54984; MUID:95007776; PMID:7522971  
 A;Accession: A54984  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-209 <CHE>  
 A;Cross-references: GB:U14941; NID:g558836; PIDN:AAA53636.1; PID:g558837  
 R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.  
 J. Biol. Chem. 270, 3467-3470, 1995  
 A;Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase ligand that is identical to the ligand (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases.  
 A;Reference number: A55873; MUID:95181289; PMID:7876076  
 A;Accession: A55873  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-209 <SHA>  
 A;Cross-references: GB:U14752; NID:g681886; PIDN:AAA68520.1; PID:g681887  
 C;Superfamily: axon guidance signal protein  
 C;Keywords: lipoprotein; membrane protein

Query Match 7.2%; Score 176; DB 2; Length 209;  
 Best Local Similarity 29.3%; Pred. No. 1.8e-05;  
 Matches 58; Conservative 19; Mismatches 69; Indels 52; Gaps 7;

```

Qy      33 VYWNSANKRFQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
        |||| :| |||      ||| :  || ||: ||  || :  || ||:| |
Db      35 VYWNRSNPRFQVSAVGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93

Qy      88 QGRRCEAPPAPNLLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGT 144
        |:      |:|      |:|: ||| :|  ||| |:| |: :
Db      94 GHASCDHRQRGFKRWE CNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYYISATP-- 151

Qy     145 REGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSLEPGKENLP 204
        :|      ||      :|| :|  | | |
Db     152 ----PNLVDRPCLR--LKVYVR-----PTNETLY 174

Qy     205 GDP----TSNATSRGAEG 218
        |      |||:|  | |
Db     175 EAPEPIFTSNSSCSGLGG 192

```

# RESULT 9

JE0322

ephrin-A2 - human

C;Species: Homo sapiens (man)

C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000

C;Accession: JE0322

R;Aasheim, H.; Pedoutour, F.; Grosgeorge, J.; Logtenberg, T.

Biochem. Biophys. Res. Commun. 252, 378-382, 1998

A;Title: Cloning, chromosomal mapping, and tissue expression of the gene encoding the human Eph-family kinase ligand ephrin-A2.

A;Reference number: JE0322; MUID:99045414; PMID:9826538  
A;Accession: JE0322  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-213 <AAS>  
A;Cross-references: GB:AJ007292; NID:g3688367; PIDN:CAA07435.1; PID:g3688368  
C;Superfamily: axon guidance signal protein

Query Match 7.2%; Score 175.5; DB 2; Length 213;  
Best Local Similarity 36.8%; Pred. No. 2e-05;  
Matches 43; Conservative 14; Mismatches 51; Indels 9; Gaps 3;

QY 33 VYWSANKRFQA-----EGGYVLYPQIGDRDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87  
| | | | : | | | | | | : | | | | : | | | | |  
Db 39 VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97  
  
QY 88 QGRRCEAPPAPNLLLTCDRDL---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATS 141  
| : | : | | | : | | | : | | | : | :  
Db 98 GHASCDHRQRGFKRWEENRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISAT 154

#### RESULT 10

A57084

repulsive axon guidance signal protein RAGS precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 03-Nov-1995 #sequence\_revision 03-Nov-1995 #text\_change 20-Jun-2000

C;Accession: A57084

R;Drescher, U.; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, M.;  
Bonhoeffer, F.

Cell 82, 359-370, 1995

A;Title: In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa  
tectal protein related to ligands for Eph receptor tyrosine kinases.

A;Reference number: A57084; MUID:95360980; PMID:7634326

A;Accession: A57084

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-228 <DRE>

A;Cross-references: GB:X90377; NID:g1061113; PIDN:CAA62027.1; PID:g984118

C;Superfamily: axon guidance signal protein

C;Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage

F;1-20/Domain: signal sequence #status predicted <SIG>

Query Match 7.0%; Score 170.5; DB 2; Length 228;  
Best Local Similarity 28.9%; Pred. No. 4.8e-05;  
Matches 73; Conservative 30; Mismatches 91; Indels 59; Gaps 13;

QY 16 LLLLGVLGL-VSGLSLEP-----VYWSANKRFQAEGGYVLYPQIGDRDLLCPR 64  
: | | | | | | | | | | | | | | : | | : | | | : | |  
Db 6 MLLLAVALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQ-QGDYHIDVCINDYLDVFCPH 64  
  
QY 65 ARPPGPHSSPNYEFYKLYLVG-----GAQGRRCEAPPAPNLLLTCDRDLDLR 112  
| | | | | | | : | | : | | : | :  
Db 65 YEDSVPEDKT--ERYVLYMVNFDGYSSCDHISKGFKRWEENRPHSPN-----GPLK 113  
  
QY 113 FTIKFQEYSPNLWGHEFRSHHDYIIATS---DGTREGLES LQGGVCLTRGMKVLLRVGQ 169  
| : | | : | | | | : | : : : | | | : | : | : |  
Db 114 FSEKFQLFTPFSLGFEFRPGREYFYISSAIPDNGRRS-----CLK--LKV FVR--- 159

```

Qy      170 SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMP--A 227
      |      :      |      :      :      :      :      :      :      :      :
Db      160 -PANSCMKTIGVHDRVFDVNDKVENSLPADDTV--RESAEPSRG-ENAAQTPRIPIRL 214

Qy      228 VAGAAGGLALLLL 240
      :|      ||:|:
Db      215 LATLLFLLAMLLI 227

```

RESULT 11

I38850

LERK-4 - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text change 29-Sep-1999

C;Accession: I38850

R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.;  
Lyman, S.D.; Srinivasan, S.; Fletcher, F.A.; Gayle, R.B.

Oncogene 10, 299-306, 1995

A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encoding a family of proteins.

A;Reference number: I38849; MUID:95140419; PMID:7838529

A;Accession: I38850

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-201 <RES>

A;Cross-references: EMBL:U14188; NID:g642834; PIDN:AAC50079.1; PID:g642835

C;Genetics:

A; Gene: GDB:EPLG4

A;Cross-references: GDB:438337; OMIM:601380

A;Map position: 1q21-1q22

C;Superfamily: axon guidance signal protein

Query Match 6.9%; Score 169.5; DB 2; Length 201;

Best Local Similarity 29.9%; Pred. No. 5e-05;

Matches 66; Conservative 18; Mismatches 82; Indels 55; Gaps 10;

QY 24 LVSGLSL-EPVYWSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82  
| | || ||||:| | |: :| ||::|| || | | : ||  
Db 20 LRGSSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76

QY 83 LVGGAQGRCEAP-PAPNLLLTCDRPDLRLFTIKFQEYSPNLWGHEFRSHHDYIIATS 141  
:| :| | | | ::| | :| | | | :  
Db 77 MVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTFSLGFEFLPGETYYYYISVP 136

Qy 142 DGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAANSLEPGKE 201  
 | | | | | | | | | | | | | | : | :  
 Db 137 --TPE-----SSGQCL-----RLQVSVCCCKERKSES AHPV----- 164

```
Qy      202 NLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240
          | | : || || : | |                               | |||
Db      165 ---GSPGESGTSGWRGGDTPSP-----LCLLLL 189
```

RESULT 12

I58170

LERK-7 precursor - human

N;Alternate names: AL-1  
 C;Species: Homo sapiens (man)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 29-Sep-1999  
 C;Accession: I58170; G01812  
 R;Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.;  
 Tsai, S.P.; Goddard, A.; Henzel, W.J.; Hefti, F.  
 Neuron 14, 973-981, 1995  
 A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor  
 involved in axon bundle formation.  
 A;Reference number: I58170; MUID:95267434; PMID:7748564  
 A;Accession: I58170  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-228 <RES>  
 A;Cross-references: GB:S77167; NID:g914184; PID:g914185  
 R;Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K.  
 submitted to the EMBL Data Library, May 1995  
 A;Reference number: G08477  
 A;Accession: G01812  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-228 <KOZ>  
 A;Cross-references: EMBL:U26403; NID:g1019430; PIDN:AAB60377.1; PID:g1019431  
 C;Genetics:  
 A;Gene: GDB:EPLG7; AF1; LERK7  
 A;Cross-references: GDB:568757; OMIM:601535  
 A;Map position: 13q33-13q33  
 C;Superfamily: axon guidance signal protein

Query Match 6.8%; Score 167.5; DB 2; Length 228;  
 Best Local Similarity 28.8%; Pred. No. 7.9e-05;  
 Matches 65; Conservative 29; Mismatches 81; Indels 51; Gaps 11;

```

Qy      33 VYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG----- 85
        |||||:| ||| | | : | | ||: || | | | | :|
Db      34 VYWNSSNPRFQ--RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC 90

Qy      86 -----GAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYIIAT 140
        | : | | :|| | :| ||| :| | || | :| :|
Db      91 DHTSKGFKRWECNRPHSPN-----GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS 141

Qy      141 S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAHSLE 197
        : :| | | | | :|| :| | : | : | : | :|
Db      142 AIPDNRRS-----CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSL 186

Qy      198 PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGCLALLLLGVA 243
        | : : | ||| | | :| : ||| :|
Db      187 PADDTV---HESAEPSRG-ENAAQTPRIPSRL-----LAILLFLLA 223

```

# RESULT 13

A36377

B61 protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 29-Sep-1999

C;Accession: A36377

R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.

Mol. Cell. Biol. 10, 5830-5838, 1990

A;Title: A novel immediate-early response gene of endothelium is induced by cytokines and encodes a secreted protein.

A;Reference number: A36377; MUID:91042512; PMID:2233719

A;Accession: A36377

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-205 <HOL>

A;Cross-references: GB:M57730; GB:M37476; NID:g179320; PIDN:AAA58388.1; PID:g179321

C;Superfamily: axon guidance signal protein

Query Match 6.8%; Score 166; DB 2; Length 205;  
Best Local Similarity 27.5%; Pred. No. 9e-05;  
Matches 46; Conservative 31; Mismatches 74; Indels 16; Gaps 5;

```
QY      18 LLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDLLCPRARPPGPHSSPN-- 75
      |||:  ::  |:|||:| :|: | | :: |: | :|::||  || :
Db       8 LLGLCCSLAAADRHTVFWNSSNPKEFNE-DYTIHVQLNDYVDIICPHYE---DHSVADAA 63

QY      76 YEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSH 132
      | | ||||  : : |:  :  |:||  : : ||| :| | ||:
Db       64 MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFPTFTLGKEFKEG 123

QY     133 HDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
      | || |:  |  ||  : | : : ||:  |::
Db     124 HSYYYISKPIHQHEDR-----CLRLKVTVSGKITHSPQAHVNPQE 163
```

#### RESULT 14

S31216

collagen alpha 1(X) chain precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999

C;Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830

R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; Cheah, K.S.E.

Eur. J. Biochem. 213, 99-111, 1993

A;Title: Intron-exon structure, alternative use of promoter and expression of the mouse collagen X gene, Coll10a-1.

A;Reference number: S31216; MUID:93238750; PMID:8477738

A;Accession: S31216

A;Molecule type: DNA

A;Residues: 1-680 <KON>

A;Cross-references: EMBL:Z21610; NID:g49793; PIDN:CAA79736.1; PID:g49794

R;Elima, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Crombrughe, B.; Vuorio, E.

Biochem. J. 289, 247-253, 1993

A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and expression pattern.

A;Reference number: S28807; MUID:93143676; PMID:8424763

A;Accession: S28807

A;Molecule type: DNA

A;Residues: 1-285, 'A', 287-680 <ELI>

A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481

R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Crombrughe, B.; Vuorio, E.

Biochim. Biophys. Acta 1130, 78-80, 1992  
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRNAs.  
A;Reference number: S22215; MUID:92182017; PMID:1543751  
A;Accession: S22215  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 385-450, 'K', 452-627 <ELA>  
A;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1; PID:g49796  
R;Apte, S.S.; Olsen, B.R.  
Matrix 13, 165-179, 1993  
A;Title: Characterization of the mouse type X collagen gene.  
A;Reference number: S30127; MUID:93261348; PMID:8492743  
A;Accession: S30127  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-12, 'F', 14-26, 'S', 28-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-566, 'C', 568, 'H', 570, 'IY', 573-634, 'T', 636-680 <APT>  
R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.  
Eur. J. Biochem. 206, 217-224, 1992  
A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse type X collagen gene to chromosome 10.  
A;Reference number: I48299; MUID:92267014; PMID:1587271  
A;Accession: I48299  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 52-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-566, 'C', 568, 'H', 570, 'IY', 573-634, 'T', 636-680 <RES>  
A;Cross-references: EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031  
R;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.  
J. Biol. Chem. 263, 581-587, 1988  
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibody to the amino-terminal domain.  
A;Reference number: S26397; MUID:88087150; PMID:2826450  
A;Accession: S26397  
A;Molecule type: protein  
A;Residues: 'SDGYFSQ', 24-26, 'KQ' <SUM>  
C;Genetics:  
A;Gene: Coll10a-1  
A;Map position: 10  
A;Introns: 51/3  
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology  
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>  
F;553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 6.5%; Score 159; DB 2; Length 680;  
Best Local Similarity 25.5%; Pred. No. 0.0011;  
Matches 97; Conservative 30; Mismatches 108; Indels 146; Gaps 24;

QY 1 MGPPHSGPGGV-RVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLVPQIGDRLD 59  
: ||| || || | | | : : | | |  
Db 211 IGPP--GPSGVGRRGENGFPGQPGI-----KGDRGFPGEMG----- 244  
QY 60 LLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQE 119

```

      : |||| |      | ||| |      | : : :| :
Db    245 ----PSGPPGPQGPP-----GKQGR--EGIGKPGAIGSPGQPGI----- 277
QY    120 YSPNLWGHEFRSHHDYIIATSDGT---REGLESLOGGVCLTRGMKVLLRVGQSPRGGA 175
      |  ||      || |      :|| | :|      ||      | |
Db    278 --PGEKGHPGSPG-----IAGPPGAPGFGKQGLPGLRG---QRG-----PAG-- 314
QY    176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNAISRGAEGPLPPPSMPAVAGAAGGL 235
      :| | :      : :|| |      ||: ||| |      : | :|| |      : || | :
Db    315 LPGAPGA---KGERGPAG--HPGEPGLPGSP---GNMGPQGPKGIPGNHGIPGAKGEI 364
QY    236 ALLLLGVAGAGGAMCWRRRRAKP---SES RHPG-----PGSFGRGGS LGLGGGGG 282
      | :| || || | | |      :: :||      || | : | | :|| |
Db    365 G--LVGPAGPPGA---RGARGPPGLDGKTGYPGEPGLNGPKGNPGLPGQKGDPGVGGTPG 419
QY    283 M-----GPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVY 323
      :      ||| ||| |      | || | :      || | :|
Db    420 LRGPVGPVGAKGVPGHNGEAGPR-GEPIGPTR----GPTGPPGVPGFPGSKGDPGNP-- 472
QY    324 IVQDGP-----PQSPP 334
      ||      | ||
Db    473 -GAPGPAGIATKGLNGPTGPP 492

```

# RESULT 15

CGBO7S

collagen alpha 1(III) chain - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 07-May-1999

C;Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946

R;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K. Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979

A;Title: The covalent structure of calf skin type III collagen. I. The amino acid sequence of the amino terminal region of the alpha1(III) chain (position 1-222).

A;Reference number: A02862; MUID:80026026; PMID:488906

A;Accession: A02862

A;Molecule type: protein

A;Residues: 1-242 <FIE>

R;Dewes, H.; Fietzek, P.P.; Kuehn, K.

Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979

A;Title: The covalent structure of calf skin type III collagen. II. The amino acid sequence of the cyanogen bromide peptide alpha1(III)CB1,8,10,2 (positions 223-402).

A;Reference number: A38001; MUID:80026027; PMID:488907

A;Accession: A38001

A;Molecule type: protein

A;Residues: 243-422 <DEW1>

R;Bentz, H.; Fietzek, P.P.; Kuehn, K.

Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979

A;Title: The covalent structure of calf skin type III collagen. III. The amino acid sequence of the cyanogen bromide peptide alpha1(III)CB4 (positions 403-551).

A;Reference number: A38002; MUID:80026028; PMID:488908

A;Accession: A38002

A;Molecule type: protein

A;Residues: 423-571 <BEN>

R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.  
 Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979  
 A;Title: The covalent structure of calf skin type III collagen. IV. The amino  
 acid sequence of the cyanogen bromide peptide alphas(III)CB5 (positions 552-  
 788).  
 A;Reference number: A38003; MUID:80026029; PMID:488909  
 A;Accession: A38003  
 A;Molecule type: protein  
 A;Residues: 572-808 <LAN>  
 R;Dewes, H.; Fietzek, P.P.; Kuehn, K.  
 Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979  
 A;Title: The covalent structure of calf skin type III collagen. V. The amino  
 acid sequence of the cyanogen bromide peptide alphas(III)CB9A (position 789 to  
 927).  
 A;Reference number: A38004; MUID:80026030; PMID:488910  
 A;Accession: A38004  
 A;Molecule type: protein  
 A;Residues: 809-947 <DEW2>  
 R;Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.  
 Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979  
 A;Title: The covalent structure of calf skin type III collagen. VI. The amino  
 acid sequence of the carboxyterminal cyanogen bromide peptide alphas(III)CB9B  
 (position 928-1028).  
 A;Reference number: A38005; MUID:80026031; PMID:488911  
 A;Accession: A38005  
 A;Molecule type: protein  
 A;Residues: 948-1049 <ALL>  
 A;Experimental source: skin  
 R;Henkel, W.  
 Biochem. J. 318, 497-503, 1996  
 A;Title: Cross-link analysis of the C-telopeptide domain from type III collagen.  
 A;Reference number: S71946; MUID:96404897; PMID:8809038  
 A;Accession: S71946  
 A;Molecule type: protein  
 A;Residues: 87-106;1017-1029;1037-1049 <HEN>  
 C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-  
 Y) are hydroxylated in some or all of the chains.  
 C;Comment: The type III collagen molecule is a trimer of identical chains,  
 linked to each other by interchain disulfide bonds. Trimers are also cross-  
 linked by allysines forming desmosine.  
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal  
 homology; von Willebrand factor type C repeat homology  
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine;  
 hydroxyproline; skin; trimer; triple helix  
 F;1-1049/Product: collagen alpha 1(III) chain #status experimental <CAB>  
 F;1-14/Region: amino-terminal nonhelical telopeptide  
 F;15-1040/Region: helical  
 F;587-589/Region: cell attachment (R-G-D) motif  
 F;752-754/Region: cell attachment (R-G-D) motif  
 F;875-877/Region: cell attachment (R-G-D) motif  
 F;878-880/Region: cell attachment (R-G-D) motif  
 F;935-937/Region: cell attachment (R-G-D) motif  
 F;1041-1049/Region: carboxyl-terminal nonhelical telopeptide  
 F;95,107,119,938,950/Modified site: 5-hydroxylysine (Lys) #status experimental  
 F;107,950/Modified site: allysine (Lys) #status predicted  
 F;107/Binding site: carbohydrate (Lys) (covalent) #status experimental  
 F;1040,1041/Disulfide bonds: interchain #status predicted



Query Match 6.3%; Score 154.5; DB 1; Length 1049;  
Best Local Similarity 26.5%; Pred. No. 0.0036;  
Matches 60; Conservative 9; Mismatches 74; Indels 83; Gaps 8;

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QY      171 PRGGAVPRKPVSEMPMERDRGA-----AHSLEPGKEN 202  
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Db      688 PAGGSGPAGPPGPQG VKGERGSPGGPGAAGFP GGRGPPGPPGSNGNPGPPGSSGAPGKD G 747  
  
QY      203 LPGDPTSNAT-----SRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGA 245  
        || | ||                ||| || | | | | | | | |  
Db      748 PPGPPGSNGAPGSPGISGPKGDSGPPGERGAPGPQGPPGAPGLGIAG-----LTGARGL 802  
  
QY      246 GGAMCWRRRRAKP-----SES RHPGP-----GSFGRGSSLGLGGGGGMGPREAEPGE 292  
        |          | | : |||           | | | | | | | | : | |  
Db      803 AGPPGMPGARGSPGPQGIKGENGKPGPSGQNGERGPPGPQLPGLAGTAGEPGRDGNPGS 862  
  
QY      293 LGIALRGG-----GAADPPFCPHYEKVSGDYGHVPVYIVQDGPP 330  
        |: | |       |   | |         | |||     |||  
Db      863 DGLPGRDGAPGAKGDRGENSGPGAP-----GAPGHP-----GPP 896
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Search completed: September 15, 2004, 12:40:09  
Job time : 31.761 secs

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:39:22 ; Search time 99.5849 Seconds  
(without alignments)  
1465.220 Million cell updates/sec

Title: US-10-021-121-2  
Perfect score: 2450  
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%	Query
No.	Score	Match Length DB ID Description

1	2450	100.0	455	13	US-10-021-121-2	Sequence 2, Appli
2	1841	75.1	340	13	US-10-021-121-4	Sequence 4, Appli
3	1837	75.0	340	13	US-10-138-787-3	Sequence 3, Appli
4	1835	74.9	340	15	US-10-417-924A-2	Sequence 2, Appli
5	1550	63.3	285	16	US-10-408-765A-2695	Sequence 2695, Ap
6	623	25.4	346	13	US-10-021-121-9	Sequence 9, Appli
7	623	25.4	346	16	US-10-356-289-2	Sequence 2, Appli
8	620.5	25.3	333	9	US-09-754-105-2	Sequence 2, Appli
9	620.5	25.3	333	9	US-09-978-339-2	Sequence 2, Appli
10	620.5	25.3	333	13	US-10-021-121-10	Sequence 10, Appl
11	620.5	25.3	333	15	US-10-331-496A-63	Sequence 63, Appl
12	613.5	25.0	333	13	US-10-138-787-4	Sequence 4, Appli
13	599.5	24.5	345	13	US-10-138-787-5	Sequence 5, Appli
14	489	20.0	89	9	US-09-862-179A-17	Sequence 17, Appl
15	489	20.0	89	13	US-10-138-787-13	Sequence 13, Appl
16	284.5	11.6	92	9	US-09-864-761-48262	Sequence 48262, A
17	196.5	8.0	136	9	US-09-864-761-48257	Sequence 48257, A
18	193.5	7.9	106	9	US-09-925-297-639	Sequence 639, App
19	192	7.8	82	9	US-09-862-179A-15	Sequence 15, Appl
20	192	7.8	82	13	US-10-138-787-11	Sequence 11, Appl
21	191.5	7.8	82	9	US-09-862-179A-16	Sequence 16, Appl
22	191.5	7.8	82	13	US-10-138-787-12	Sequence 12, Appl
23	179	7.3	238	9	US-09-904-954-2	Sequence 2, Appli
24	179	7.3	238	10	US-09-733-756-2	Sequence 2, Appli
25	179	7.3	238	14	US-10-241-220-72	Sequence 72, Appl
26	179	7.3	238	15	US-10-295-027-130	Sequence 130, App
27	176	7.2	209	9	US-09-921-984-2	Sequence 2, Appli
28	174.5	7.1	233	13	US-10-138-787-7	Sequence 7, Appli
29	172.5	7.0	218	9	US-09-925-297-510	Sequence 510, App
30	169.5	6.9	201	9	US-09-904-954-4	Sequence 4, Appli
31	169.5	6.9	225	16	US-10-322-696-135	Sequence 135, App
32	169	6.9	201	13	US-10-138-787-8	Sequence 8, Appli
33	168.5	6.9	209	13	US-10-138-787-6	Sequence 6, Appli
34	167.5	6.8	228	8	US-08-578-684-4	Sequence 4, Appli
35	166	6.8	205	13	US-10-138-787-10	Sequence 10, Appl
36	166	6.8	205	14	US-10-171-311-50	Sequence 50, Appl
37	166	6.8	205	15	US-10-372-683-34	Sequence 34, Appl
38	164.5	6.7	204	12	US-10-147-493-288	Sequence 288, App
39	164.5	6.7	204	12	US-10-145-127-288	Sequence 288, App
40	164.5	6.7	204	12	US-10-160-503-288	Sequence 288, App
41	164.5	6.7	204	12	US-10-143-118-288	Sequence 288, App
42	164.5	6.7	204	12	US-10-144-993-288	Sequence 288, App
43	164.5	6.7	204	12	US-10-158-787-288	Sequence 288, App
44	164.5	6.7	204	12	US-10-140-024-288	Sequence 288, App
45	164.5	6.7	204	12	US-10-140-808-288	Sequence 288, App

#### ALIGNMENTS

RESULT 1  
 US-10-021-121-2  
 ; Sequence 2, Application US/10021121  
 ; Publication No. US20020142444A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Caras, Ingrid W

```

; TITLE OF INVENTION: A2-1 Neurotrophic Factor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/021,121
; FILING DATE: 06-Dec-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,130
; FILING DATE: 19-Mar-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1001
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-021-121-2

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Query Match          100.0%; Score 2450; DB 13; Length 455;
Best Local Similarity 100.0%; Pred. No. 7.6e-187;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
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Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

QY     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
      |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

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Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

QY    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

QY    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGMPREAEPEGELGIALRGG 300

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Db      241  |||||GVAGAGGAMCWRRRRAKPSSESRHPGPSFGRGSSLGLGGGGMGMPREAEPEGELGIALRGG 300
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QY      361  CSRVTTFLFPVQVITTSTCRMTSFSFSTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420
Db      361  |||||CSRVTTFLFPVQVITTSTCRMTSFSFSTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420
QY      421  VLVLLLLLGRNLNMHQTLLRQRASVEAEAGQHGPL 455
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RESULT 2

US-10-021-121-4

; Sequence 4, Application US/10021121

; Publication No. US20020142444A1

; GENERAL INFORMATION:

; APPLICANT: Caras, Ingrid W

; TITLE OF INVENTION: A2-1 Neurotrophic Factor

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/021,121

; FILING DATE: 06-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/635,130

; FILING DATE: 19-Mar-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, PhD., Timothy E.

; REGISTRATION NUMBER: 36,700

; REFERENCE/DOCKET NUMBER: P1001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 340 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-021-121-4

Query Match 75.1%; Score 1841; DB 13; Length 340;  
Best Local Similarity 100.0%; Pred. No. 1.9e-138;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
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Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLRFTIKFQEY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
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Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSESRRHPGPSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300
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Db    241 GVAGAGGAMCWRRRRRAKPSESRRHPGPSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
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RESULT 3

US-10-138-787-3

; Sequence 3, Application US/10138787

; Publication No. US20020172984A1

; GENERAL INFORMATION:

; APPLICANT: Holland, Sacha

; APPLICANT: Mbamalu, Geraldine

; APPLICANT: Pawson, Tony

; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED

; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

; TITLE OF INVENTION: TYROSINE KINASES

; FILE REFERENCE: 11757.23USWO

; CURRENT APPLICATION NUMBER: US/10/138,787

; CURRENT FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US/09/214,631

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: PCT/CA97/00473

; PRIOR FILING DATE: 1997-07-04

; PRIOR APPLICATION NUMBER: 60/021,272

; PRIOR FILING DATE: 1996-07-05

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 340

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-138-787-3

Query Match 75.0%; Score 1837; DB 13; Length 340;  
Best Local Similarity 99.7%; Pred. No. 4.1e-138;  
Matches 337; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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      |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

QY    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180
      |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLQVGQSPRGGA VPRKP 180

QY    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

QY    241 GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300
      |||
Db    241 GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300

QY    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
      |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 4

US-10-417-924A-2

; Sequence 2, Application US/10417924A

; Publication No. US20030215918A1

; GENERAL INFORMATION:

; APPLICANT: Samuel Davis, et al.

; TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS

; FILE REFERENCE: REG-341Z

; CURRENT APPLICATION NUMBER: US/10/417,924A

; CURRENT FILING DATE: 2003-04-17

; PRIOR APPLICATION NUMBER: 09/051,994

; PRIOR FILING DATE: 1998-04-24

; PRIOR APPLICATION NUMBER: PCT/US96/17201

; PRIOR FILING DATE: 1996-10-25

; PRIOR APPLICATION NUMBER: 60/007,015

; PRIOR FILING DATE: 1995-10-25

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 340

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: Misc. feature

; LOCATION: (166)

; OTHER INFORMATION: Xaa = unknown or other

US-10-417-924A-2

Query Match 74.9%; Score 1835; DB 15; Length 340;  
Best Local Similarity 99.7%; Pred. No. 5.9e-138;  
Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
          |||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

QY     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
          |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

QY    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180
          |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180

QY    181 VSEMPMERDRGA AHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          |||
Db    181 VSEMPMERDRGA AHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

QY    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300
          |||
Db    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300

QY    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
          |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 5

US-10-408-765A-2695

; Sequence 2695, Application US/10408765A

; Publication No. US20040101874A1

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Fahy, Eoin D.

; APPLICANT: Zhang, Bing

; APPLICANT: Gibson, Bradford W.

; APPLICANT: Taylor, Steven W.

; APPLICANT: Glenn, Gary M.

; APPLICANT: Warnock, Dale E.

; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

; FILE REFERENCE: 660088.465

; CURRENT APPLICATION NUMBER: US/10/408,765A

; CURRENT FILING DATE: 2003-04-04

; NUMBER OF SEQ ID NOS: 3077

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2695

; LENGTH: 285

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-2695

Query Match 63.3%; Score 1550; DB 16; Length 285;  
Best Local Similarity 100.0%; Pred. No. 2.5e-115;



Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      56 DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPLDLRFTI 115
      |||
Db      1 DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPLDLRFTI 60

Qy     116 KFQEYSPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA 175
      |||
Db      61 KFQEYSPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA 120

Qy     176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 235
      |||
Db     121 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 180

Qy     236 ALLLLGVAGAGGAMCWRRRRAKPSERHPGPGSFGRGSLGLGGGGMGPREAEPGELGI 295
      |||
Db     181 ALLLLGVAGAGGAMCWRRRRAKPSERHPGPGSFGRGSLGLGGGGMGPREAEPGELGI 240

Qy     296 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNIIY 338
      |||
Db     241 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNIIY 283
```

RESULT 6

US-10-021-121-9

; Sequence 9, Application US/10021121

; Publication No. US20020142444A1

; GENERAL INFORMATION:

; APPLICANT: Caras, Ingrid W  
; TITLE OF INVENTION: A2-1 Neurotrophic Factor  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/021,121  
; FILING DATE: 06-Dec-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/635,130  
; FILING DATE: 19-Mar-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, PhD., Timothy E.  
; REGISTRATION NUMBER: 36,700  
; REFERENCE/DOCKET NUMBER: P1001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 346 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
 US-10-021-121-9

Query Match 25.4%; Score 623; DB 13; Length 346;  
 Best Local Similarity 39.2%; Pred. No. 2.7e-41;  
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY	8	PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLL	61
		:   :  : :   :     :   :  :   :  :    : :	
Db	4	PGQRWLGKWLVMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII	63
QY	62	CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRDLRLFTIKFQEYS	121
		:           :    : : :       :	
Db	64	CPRAEAGRP-----YEEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS	118
QY	122	PNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGA VPRKPV	181
		:       :  : :     : :         :::       :	
Db	119	PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTMTMKIIMKVGQDPNAVTPQEQLTT	178
QY	182	SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----	236
		: :       :     :   :  :	
Db	179	SRPSKEADNTVKMATQAPGSRGSLGDSGKHETVNTQEEKSGP-----GASGGSSGDPD	231
QY	237	-----LLLLGVAGAGGA-----MCWRRRRRAKPSERHPGPGSFRGGSLGL	277
		:       :  :   :  :   :	
Db	232	GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHHTQQ-----RAAALSL	282
QY	278	----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP	333
		: :    : :                   :	
Db	283	STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP	339
QY	334	PNIIY 338	
Db	340	ANIIY 344	

# RESULT 7

US-10-356-289-2

; Sequence 2, Application US/10356289

; Publication No. US20040022767A1

## ; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; APPLICANT: Beckmann, M. Patricia

; APPLICANT: Baum, Peter R.

; APPLICANT: Carpenter, Melissa K.

; TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND

; FILE REFERENCE: GENENT.67CPDV3

; CURRENT APPLICATION NUMBER: US/10/356,289

; CURRENT FILING DATE: 2003-01-31

; PRIOR APPLICATION NUMBER: US/09/039,642B

; PRIOR FILING DATE: 1998-03-16

; PRIOR APPLICATION NUMBER: 08/213,403

; PRIOR FILING DATE: 1994-03-15  
 ; PRIOR APPLICATION NUMBER: 07/977,693  
 ; PRIOR FILING DATE: 1992-11-13  
 ; PRIOR APPLICATION NUMBER: 08/747,240  
 ; PRIOR FILING DATE: 1996-10-12  
 ; PRIOR APPLICATION NUMBER: 08/460,741  
 ; PRIOR FILING DATE: 1995-06-02  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 346  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-356-289-2

Query Match 25.4%; Score 623; DB 16; Length 346;  
 Best Local Similarity 39.2%; Pred. No. 2.7e-41;  
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 61  
 || :| |: |: : | :||| |:| |:| :| |:|:|:|:|:|:  
 Db 4 PGQRWLKGWLVMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63  
 QY 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPDLDLRFITKFEYS 121  
 |||| | ||:||||| | | ||:|:|:|:|:|:|:|:|:  
 Db 64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFEFS 118  
 QY 122 PNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181  
 || | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTMTMKIIMKVGQDPNAVTPQLTT 178  
 QY 182 SEMP MERDRGAHSLE-PGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLA---- 236  
 | | | : : || || : | | ||:|:|:  
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGDSGKHETVNQEEKSGP-----GASGGSSGDPD 231  
 QY 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGSLGL 277  
 : | ||| : |:| | : | :| |  
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALSL 282  
 QY 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333  
 || | || : : || : :|:|:|:|:|:|:|:|:|:|:|:  
 Db 283 STLASPKGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339  
 QY 334 PNIYY 338  
 ||||  
 Db 340 ANIYY 344

# RESULT 8

US-09-754-105-2

; Sequence 2, Application US/09754105  
 ; Patent No. US20010009768A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cerretti, Douglas  
 ; APPLICANT: Reddy, Pranhitha  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5  
 ; FILE REFERENCE: 28232

```
; CURRENT APPLICATION NUMBER: US/09/754,105
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 09/329,531
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-754-105-2
```

```
Query Match          25.3%; Score 620.5; DB 9; Length 333;
Best Local Similarity 40.5%; Pred. No. 4.1e-41;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;
```

```
Qy      14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||::|::|: :
Db      14 GVLMLVCRTAISKISIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV--DSKTV 70

Qy      74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLLTCDRPDLDLRFITIKFQEYSPNLWGHEFRSHH 133
      ||::|:|:| | || || | :|| |::| |||||:| |||| | : :
Db      71 GQY EYKVMVDKQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy     134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      ||||:|:|:| |::: :||| || |:::| || | : | :|
Db     131 DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy     191 GAAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | : : : : : || | | : : : :
Db     191 GRSSTTSPFVKPNPGSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy     251 WRRRRRAKPSESRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
      ||| : :| | : : | :|| : : | || || |||
Db     251 KYRRRHRKHSPQHTTTLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy     311 YEKVSGDYGHPVYIVQDGPQSPPNIIY 338
      ||||| ||||| ||||| : |||| | |||
Db     304 YEKVSGDYGHPVYIVQEMPPQSPANIY 331
```

# RESULT 9

US-09-978-339-2

; Sequence 2, Application US/09978339

; Patent No. US20020103358A1

; GENERAL INFORMATION:

; APPLICANT: Cerretti, Douglas P.

; Reddy, Pranhitha

; TITLE OF INVENTION: No. US20020103358A1el Cytokine Designated Lerk-5

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98101

```

;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: Apple Macintosh
;      OPERATING SYSTEM: Apple 7.1
;      SOFTWARE: Microsoft Word, Version 5.1a
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/978,339
;      FILING DATE: 15-Oct-2001
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/271,948
;      FILING DATE: <Unknown>
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Seese, Kathryn A.
;      REGISTRATION NUMBER: 32,172
;      REFERENCE/DOCKET NUMBER: 2823
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206) 587-0430
;      TELEFAX: (206) 233-0644
;      TELEX: 756822
;
;      INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 333 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-978-339-2

```

```

Query Match          25.3%; Score 620.5; DB 9; Length 333;
Best Local Similarity 40.5%; Pred. No. 4.1e-41;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

```

```

Qy      14 GALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::|: :
Db      14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy      74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133
      ||::|:|:| | || || | :|| |::| |||||:| |||| | : :
Db      71 GQYEYYKVYMDKQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy      134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      |||||:|:|:| |||: :||| || ||:|:| || | | : | :|
Db      131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy      191 GAAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | : : : : : : || | | : : : :
Db      191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy      251 WRRRRRAKPSESRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
      ||| : :| | : : | :|| : : | || || |||
Db      251 KYRRRRHRKHSPQHTTTLSTLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy      311 YEKVSGDYGHPVYIVQDGPPQSPNIIY 338
      |||||:| ||||| ||||
Db      304 YEKVSGDYGHPVYIVQEMPPQSPANIIY 331

```

RESULT 10  
 US-10-021-121-10  
 ; Sequence 10, Application US/10021121  
 ; Publication No. US20020142444A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Caras, Ingrid W  
 ; TITLE OF INVENTION: A2-1 Neurotrophic Factor  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/021,121  
 ; FILING DATE: 06-Dec-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/635,130  
 ; FILING DATE: 19-Mar-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Torchia, PhD., Timothy E.  
 ; REGISTRATION NUMBER: 36,700  
 ; REFERENCE/DOCKET NUMBER: P1001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-8674  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 333 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
 US-10-021-121-10

Query Match 25.3%; Score 620.5; DB 13; Length 333;  
 Best Local Similarity 40.5%; Pred. No. 4.1e-41;  
 Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWNSSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73  
 | |::| : : ||:||||:| :| | |||||::|:::| :  
 Db 14 GVLMVLCRTAISKSIIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70  
 Qy 74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133  
 ||::|::| | || || | :|| ::|||::|::| | : :  
 Db 71 GQY EYYKVYMVVDKDKQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130  
 Qy 134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190  
 ||||::|::| ||::: :||| || ||:|::|| | | : | :|

Db 131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250  
| : : | : || | : : : : : || | | : : : : :

Db 191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy 251 WRRRRRAKPSESRRHPGPGSFGRRGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310  
||| : :| | : | : || : : | || || |||

Db 251 KYRRRRHRKHSPQHTTTLSTLATPKRSGNN----NGSEPSDIIPLR---TADSVFCPH 303

Qy 311 YEKVSGDYGHPVYIVQDGPQSPNNIYY 338  
||||||| : |||| |||

Db 304 YEKVSGDYGHPVYIVQEMPQSPANNIYY 331

RESULT 11

US-10-331-496A-63

; Sequence 63, Application US/10331496A

; Publication No. US20030228305A1

; GENERAL INFORMATION:

; APPLICANT: FRANTZ, GRETCHEN

; APPLICANT: HILLAN, KENNETH J.

; APPLICANT: PHILLIPS, HEIDI S.

; APPLICANT: POLAKIS, PAUL

; APPLICANT: SMITH, VICTORIA

; APPLICANT: SPENCER, SUSAN D.

; APPLICANT: WILLIAMS, P. MICKEY

; APPLICANT: WU, THOMAS D.

; APPLICANT: ZHANG, ZEMIN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TITLE OF INVENTION: TREATMENT OF TUMOR

; FILE REFERENCE: P5014R1-PCT

; CURRENT APPLICATION NUMBER: US/10/331,496A

; CURRENT FILING DATE: 2002-12-30

; PRIOR APPLICATION NUMBER: US 60/345,444

; PRIOR FILING DATE: 2002-01-02

; PRIOR APPLICATION NUMBER: US 60/351,885

; PRIOR FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: US 60/360,066

; PRIOR FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: US 60/362,004

; PRIOR FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: US 60/366,869

; PRIOR FILING DATE: 2002-03-20

; PRIOR APPLICATION NUMBER: US 60/366,284

; PRIOR FILING DATE: 2002-03-21

; PRIOR APPLICATION NUMBER: US 60/368,679

; PRIOR FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: US 60/404,809

; PRIOR FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: US 60/405,645

; PRIOR FILING DATE: 2002-08-21

; NUMBER OF SEQ ID NOS: 95

; SEQ ID NO 63

; LENGTH: 333

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-331-496A-63

Query Match 25.3%; Score 620.5; DB 15; Length 333;  
Best Local Similarity 40.5%; Pred. No. 4.1e-41;  
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWSANKRFQAEGGYVLYPQIGDRLLCPRARPPGPHSS 73  
| |::| : : |||:||||:| :| | |||||:|::|: :  
Db 14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy 74 PNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLRLRFTIKFQEYSPNLWGHEFRSHH 133  
||:|:|:| | || || | :|| |:|||||:||||| ||: :  
Db 71 GQYEEYKVMVDKDQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy 134 DYYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190  
||||:|:|:| |||:: :||| || |:|:| || | : | :|  
Db 131 DYYIIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250  
| : : | : || | : : : : : || | | : : : : :  
Db 191 GRSSTTSPFVKPNPGSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy 251 WRRRRRAKPSESRRHPGPSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310  
||| : :| | : | :|| :| :| || || |||  
Db 251 KYRRRRHRKHSPQHTTTLSTLSTLATPKRSGNN---NGSEPSDIIIPLR---TADSVFCPH 303

Qy 311 YEKVSGDYGHPVYIVQDGPPQSPPNIIY 338  
|||||||||||||||: |||| ||||  
Db 304 YEKVSGDYGHPVYIVQEMPPQSPANIIY 331

RESULT 12

US-10-138-787-4

; Sequence 4, Application US/10138787  
; Publication No. US20020172984A1  
; GENERAL INFORMATION:  
; APPLICANT: Holland, Sacha  
; APPLICANT: Mbamalu, Geraldine  
; APPLICANT: Pawson, Tony  
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED  
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR  
; TITLE OF INVENTION: TYROSINE KINASES  
; FILE REFERENCE: 11757.23USWO  
; CURRENT APPLICATION NUMBER: US/10/138,787  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US/09/214,631  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: PCT/CA97/00473  
; PRIOR FILING DATE: 1997-07-04  
; PRIOR APPLICATION NUMBER: 60/021,272  
; PRIOR FILING DATE: 1996-07-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 333  
; TYPE: PRT  
; ORGANISM: Homo sapiens



US-10-138-787-4

Query Match 25.0%; Score 613.5; DB 13; Length 333;  
Best Local Similarity 40.5%; Pred. No. 1.5e-40;  
Matches 133; Conservative 54; Mismatches 128; Indels 13; Gaps 6;

Qy 14 GALLLLGVLGLVSGLSLEPVYWSANKRFQAEAGGYVLYPQIGDRDLLCPRARPPGPHSS 73  
| |::| : : |||:| ||:| :| | |||||::|::|::| :  
Db 14 GVLMLCRTAISKSIVLEPIYMNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy 74 PNYEFYKLYLVGGAQGRRCCEAPPAPNLLLLTCDRPDLRLFTIKFQEYSPNLWGHEFRSHH 133  
||::|::|:| | || || | :|| |::| |||||::| ||||| ||: :  
Db 71 GQYEYKVMVDKQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy 134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ-SPRGGAVPRKPVSEMP-MER-DR 190  
||||:|::|: |||:: :||| || ||:|::| | : | : | : | :  
Db 131 DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTPNKDPTRRPELEAGTN 190

Qy 191 GAAHSLEPGKENLPGDPTSNAISRGAEGLPPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250  
| : : | : || | : : : : : || | | : : : : :  
Db 191 GRSSTTSPFVKPNPGSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy 251 WRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310  
||| : :| | : | : || :| :| || | |||  
Db 251 KYRRRRHRKHSPQHTTTLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy 311 YEKVSGDYGHPVYIVQDGPPQSPNIIYY 338  
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Db 304 YEKVSGDYGHPVYIVQEMPPQSPANIIYY 331

RESULT 13

US-10-138-787-5

; Sequence 5, Application US/10138787  
; Publication No. US20020172984A1  
; GENERAL INFORMATION:  
; APPLICANT: Holland, Sacha  
; APPLICANT: Mbamalu, Geraldine  
; APPLICANT: Pawson, Tony  
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED  
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR  
; TITLE OF INVENTION: TYROSINE KINASES  
; FILE REFERENCE: 11757.23USWO  
; CURRENT APPLICATION NUMBER: US/10/138,787  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US/09/214,631  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: PCT/CA97/00473  
; PRIOR FILING DATE: 1997-07-04  
; PRIOR APPLICATION NUMBER: 60/021,272  
; PRIOR FILING DATE: 1996-07-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-138-787-5

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Query Match          24.5%;  Score 599.5;  DB 13;  Length 345;
Best Local Similarity 38.4%;  Pred. No. 2e-39;
Matches 140;  Conservative 50;  Mismatches 116;  Indels 59;  Gaps 10;

Qy      8 PGGVRVG----ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
      ||| :|      |:::  :  | :  | :||| | :|  | :|  :  | |::|::|::|::|
Db      4 PGGRWLKGWLYAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
      || |      |      ||:|||||  |      |      | :|:|:|:|:  ::|:|:|:|:|
Db     64 CPPAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPMVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      ||  | ||:  |||||  :|:|:  |||:  :|||  ||  ||:::|  |      :
Db    119 PNYMGLEFKKHHDYIITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTP EQLT 178

Qy    182 SEMP MERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      |      | |      : : ||      ||      :  |      |      ||:|  :
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDSGKHETV NQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      :  |      |||      :  :|  | :  :      | :|  |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLPKRHRKHTQ-----RAAALSL 281

Qy    278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      || |      || : : | |      :  :|:|:|:|:|:|:|:|:|:|:|:|:|
Db    282 STIASPKGGSGTAGTEPSDIIPL---FTTENNYCPHYEKVSGDYGHPVYIVQEMP PQSP 338

Qy    334 PNIIY 338
      ||||
Db    339 ANIIY 343
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RESULT 14

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US-09-862-179A-17
; Sequence 17, Application US/09862179A
; Patent No. US20020147306A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Danny
; APPLICANT: Pawson, Anthony
; TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS
; TITLE OF INVENTION: AND PDZ DOMAINS
; FILE REFERENCE: MTSI-P01-009
; CURRENT APPLICATION NUMBER: US/09/862,179A
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-179A-17
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Query Match          20.0%;  Score 489;  DB 9;  Length 89;
Best Local Similarity 100.0%;  Pred. No. 2.4e-31;
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Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 RRRRAKPSES RHPGPGSFGRGSSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 311  
 |||  
 Db 1 RRRRAKPSES RHPGPGSFGRGSSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 60

Qy 312 EKVSGDYGHPVYIVQDGPPQSPPNIYY 338  
 |||  
 Db 61 EKVSGDYGHPVYIVQDGPPQSPPNIYY 87

RESULT 15

US-10-138-787-13

; Sequence 13, Application US/10138787

; Publication No. US20020172984A1

; GENERAL INFORMATION:

; APPLICANT: Holland, Sacha

; APPLICANT: Mbamalu, Geraldine

; APPLICANT: Pawson, Tony

; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED

; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

; TITLE OF INVENTION: TYROSINE KINASES

; FILE REFERENCE: 11757.23USWO

; CURRENT APPLICATION NUMBER: US/10/138,787

; CURRENT FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US/09/214,631

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: PCT/CA97/00473

; PRIOR FILING DATE: 1997-07-04

; PRIOR APPLICATION NUMBER: 60/021,272

; PRIOR FILING DATE: 1996-07-05

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-138-787-13

Query Match 20.0%; Score 489; DB 13; Length 89;

Best Local Similarity 100.0%; Pred. No. 2.4e-31;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 RRRRAKPSES RHPGPGSFGRGSSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 311  
 |||  
 Db 1 RRRRAKPSES RHPGPGSFGRGSSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 60

Qy 312 EKVSGDYGHPVYIVQDGPPQSPPNIYY 338  
 |||  
 Db 61 EKVSGDYGHPVYIVQDGPPQSPPNIYY 87

Search completed: September 15, 2004, 12:55:53

Job time : 101.585 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:29:25 ; Search time 88.1384 Seconds  
(without alignments)  
1628.811 Million cell updates/sec

Title: US-10-021-121-2  
Perfect score: 2450  
Sequence: 1 MGPPHSGPGGVRVGALLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

%  
Result Query  
No. Score Match Length DB ID Description  
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1	914	37.3	331	13	Q90Z31	Q90z31 brachydanio
2	910	37.1	327	13	Q9PT69	Q9pt69 xenopus lae
3	620.5	25.3	333	13	Q9PUJ4	Q9puj4 gallus gall
4	607	24.8	341	13	Q90Z33	Q90z33 brachydanio
5	596.5	24.3	334	13	Q90Z32	Q90z32 brachydanio
6	331	13.5	205	13	Q9W6H9	Q9w6h9 xenopus lae
7	214.5	8.8	237	5	Q9U3M2	Q9u3m2 caenorhabdi
8	198.5	8.1	279	5	Q9U474	Q9u474 caenorhabdi
9	192	7.8	652	5	Q9V4E1	Q9v4e1 drosophila
10	178.5	7.3	202	13	Q98TZ1	Q98tz1 gallus gall
11	168.5	6.9	205	4	Q8N578	Q8n578 homo sapien
12	167	6.8	205	11	Q9D7K8	Q9d7k8 mus musculu
13	163.5	6.7	206	11	Q9CZS8	Q9czs8 mus musculu
14	155.5	6.3	675	6	Q9N178	Q9n178 sus scrofa
15	155	6.3	229	13	O93431	O93431 brachydanio
16	153.5	6.3	217	13	Q7SY61	Q7sy61 xenopus lae
17	153.5	6.3	1691	11	Q9ESQ2	Q9esq2 mus musculu
18	151.5	6.2	1447	13	Q9IB91	Q9ib91 xenopus lae
19	150	6.1	2936	6	Q7YRK8	Q7yrk8 canis famil
20	149	6.1	325	5	O17036	O17036 caenorhabdi
21	149	6.1	569	5	Q17208	Q17208 bombyx mori
22	148.5	6.1	316	5	Q19111	Q19111 caenorhabdi
23	147	6.0	921	11	Q8BSQ4	Q8bsq4 mus musculu
24	146.5	6.0	590	5	Q86BH0	Q86bh0 drosophila
25	146.5	6.0	778	5	Q86BH1	Q86bh1 drosophila
26	146.5	6.0	792	5	Q8MT89	Q8mt89 drosophila
27	146.5	6.0	888	11	Q8CCZ8	Q8ccz8 mus musculu
28	146.5	6.0	1140	11	Q61434	Q61434 mus musculu
29	146.5	6.0	1449	13	Q802B5	Q802b5 xenopus lae
30	146.5	6.0	1491	13	Q91718	Q91718 xenopus lae
31	146.5	6.0	1491	13	Q7ZTM4	Q7ztm4 xenopus lae
32	146	6.0	675	13	Q90800	Q90800 gallus gall
33	146	6.0	1669	11	Q9QZS0	Q9qzs0 mus musculu
34	145.5	5.9	305	5	O17805	O17805 caenorhabdi
35	145.5	5.9	308	5	Q94620	Q94620 meloidogyne
36	145	5.9	680	11	Q9D0D2	Q9d0d2 mus musculu
37	144.5	5.9	309	5	Q25466	Q25466 meloidogyne
38	144.5	5.9	1269	13	Q7T2Z7	Q7t2z7 gallus gall
39	144.5	5.9	1347	4	Q96QB3	Q96qb3 homo sapien
40	144.5	5.9	1420	13	Q90W37	Q90w37 gallus gall
41	143.5	5.9	775	16	Q9F342	Q9f342 streptomyce
42	143	5.8	445	5	Q8MZ49	Q8mz49 drosophila
43	143	5.8	1684	6	Q8HYC1	Q8hyc1 canis famil
44	143	5.8	1688	6	Q866Z2	Q866z2 canis famil
45	143	5.8	1747	5	Q26640	Q26640 strongyloce

#### ALIGNMENTS

##### RESULT 1

Q90Z31

ID Q90Z31 PRELIMINARY; PRT; 331 AA.  
AC Q90Z31;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

```

DE   Ephrin B3.
GN   EFNB3.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375227; AAK64277.1; -.
DR   ZFIN; ZDB-GENE-010618-3; efnb3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
SQ   SEQUENCE    331 AA;  35638 MW;  6A5EACD509A09818 CRC64;

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Qy	10	GVRVGALLLLGLVGLVSGLSLEPVYWN	SANKRFQAEGGYVLYPQIGDRLDLLCPRARPPG	69
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Db	9	GLGILLIFLVDLLG-ITATNMEPIYWN	SLNKRFSDDKGYVLYPQIGDRLDLICPSSDPPG	67
Qy	70	PHSSPNYEFYKLYLVGG-AQGRRC	EAPPAPNLLLLTCDRPDLDLRF	128
		: :   :                         :   :   :		
Db	68	PRAPADYEYYKLYLVSSREQADRCEVT	GAPNLLLLTCDKPNSDMRFTIKFQ	127
Qy	129	FRSHHDYIIATSDGTREGLES	LQGGVCLTRGMKVLLRVGQSPRG-GAVPRKPVSEMPME	187
		: :   :               :       :         :		
Db	128	FKTNHDFYIIATSDGTRQGLESMRGGVCATQGMKVVLKVGQSPYGLPAKSPK	PDS-----	182
Qy	188	RDRGAAHSLEPGKENLPGDPTS	NAT-----SRGAEGPLPPPSMPAVAGAAGGLALLL	239
		:       :           : : :		
Db	183	-----AGRINNPNPGTGNSTHPQI	PPRGSGGENGPLPASNIAVIAGAAGGS	232
Qy	240	LGVAGAGGAMCWRRRRAKPS	ESRHPGPGSFG-----RGGSLGLGGGGMGPREAEPGEL	293
		:   :                         :   :   :   :		
Db	233	L-VTAVICVVCYRRRHAKHSESHHP-PLSLSSLTSPKRGCGGGVGGGNNG---	SEPSDI	287
Qy	294	GIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP	PNIYY	338
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Db	288	IIPLR---TSDSAYCPHYEKVSGDYGHPVYIVQEMPPQSP	PANIYY	329

ID Q9PT69 PRELIMINARY; PRT; 327 AA.  
AC Q9PT69;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Ephrin-B3 precursor.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=20099673; PubMed=10633856;  
RA Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,  
RA Wilkinson D.G., Brandli A.W.;  
RT "Comparative analysis of embryonic gene expression defines potential  
RT interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";  
RL Dev. Dyn. 216:361-373(1999).  
DR EMBL; AJ236866; CAB65511.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002086; Aldehyde\_dehydr.  
DR InterPro; IPR008972; Cupredoxin.  
DR InterPro; IPR001799; Ephrin.  
DR Pfam; PF00812; Ephrin; 1.  
DR PRINTS; PR01347; EPHRIN.  
DR ProDom; PD002533; Ephrin; 1.  
DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
DR PROSITE; PS01299; EPHRIN; 1.  
KW Signal.  
FT SIGNAL 1 24 POTENTIAL.  
SQ SEQUENCE 327 AA; 35913 MW; 4BB0FA39D4C22DCD CRC64;

Query Match 37.1%; Score 910; DB 13; Length 327;  
Best Local Similarity 60.1%; Pred. No. 2.6e-64;  
Matches 190; Conservative 30; Mismatches 82; Indels 14; Gaps 8;

Qy 25 VSGLSLEPVYWN SANKRFQ AEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLV 84  
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Db 22 ISALS LDPIYWNSSNKR FEDTEGYVLYPQIGDRLDLLCPRSEPQGPFS SPY EYKLYLV 81  
Qy 85 GGAQG-RRCEAPPAPNLLLTC DRPDLDL RFTIKFQEYSPNLWGHEFRSHHDYIIATSDG 143  
| : | ||||| ||||| |||||:|||||:| |||||  
Db 82 GTKEEMSSCSILRTPNLLLTC DRPSQDLRFTIKFQEYSPNLWGHEFQSQRDYIIATSDG 141  
Qy 144 TREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAHSL-EPGKEN 202  
| :|:|:||||| |:|||| |:|||| | ||:| | :| | :| :|  
Db 142 TMDGIETLQGGVCETKGMKVTLKVGQSPNGATPPRRPSS---AGKDSGISPSVPNPDPIN 198  
Qy 203 LPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSER 262  
: |: : ||| | |||| :| ||||| ||||| | | :| |||:| |:|  
Db 199 V-GETSGNATKTGENGPLPISHVPLVAGAAGGAALLLL-VFGVVGWVCHRRRQAKHSDTR 256  
Qy 263 HPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPV 322





Db 190 GTNGKSSTTSPFVKDHSGSSTDG--SKAGHSSILGSEVALFAGIASGCIIFIVIIITLVV 247  
 QY 248 AMCWRRRRRAKPSESRRHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGGGAADPPF 307  
 : ||| : :| | : | :|| :: || |  
 Db 248 LLLKYRRRRHRKHSPQHTTTLSTLSTLATPKRSGNN----NGSEPSDIIPLR---TADSVF 300  
 QY 308 CPHYEKVSGDYGHPVYIVQDGPPQSPNIIYY 338  
 ||||| : ||||  
 Db 301 CPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 331

RESULT 4

Q90Z33

ID Q90Z33 PRELIMINARY; PRT; 341 AA.  
 AC Q90Z33;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Ephrin Bl.  
 GN EFNBl.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21290827; PubMed=11397014;  
 RA Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,  
 RA Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;  
 RT "Morphogenesis of prechordal plate and notochord requires intact  
 RT eph/ephrin b signaling.";  
 RL Dev. Biol. 234:470-482(2001).  
 DR EMBL; AF375224; AAK64274.1; -.  
 DR ZFIN; ZDB-GENE-010618-2; efnbl.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 SQ SEQUENCE 341 AA; 37849 MW; CB922F20E0D93E94 CRC64;

Query Match 24.8%; Score 607; DB 13; Length 341;  
 Best Local Similarity 41.5%; Pred. NO. 3.5e-40;  
 Matches 139; Conservative 49; Mismatches 109; Indels 38; Gaps 11;

Qy 24 LVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYL 83  
 | : ||| | ||| | :| : | :||:|:|:|:|:| : | | |||||  
 Db 23 LPAAKSLESVWNSQNPKFVSGKGLVIYPEIGDKLDIICPK---GDMGRP-YEFYKLYL 77  
 Qy 84 VGGAQGRRC EAPPAPNLLLTCDRPDLDLRFITKFEYSPNLWGHEFRSHHDYIIATSDG 143  
 | | | | :|:|:|:|:|:| :|:|:|:|:|:| | || : ||| :|:|  
 Db 78 VKKEQAESCSTILDPNVLVTCNKPEKDIKFTIKFQEFSPNYMGLEFKRFTNYYITSTSNG 137  
 Qy 144 TREGLES LQGGVCLTRGMKVLLRVGQSPRG-----GAVPRKPVSEMPMERDRGAHSLEP 198



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      |   :   ||| ||:| | :|| ||||:|||| | |   ||:| |:| | : | |||:
Db      86 ETCHVTKSDMLLLNCDKPDQDVKFTFKFQEFSPNLWGLEFLRGKDYHIISTSNSTFEGLD 145
Qy      150 SLQGGVCLTRGMKVLLRVGQSPRGGA-----PRKPVSEMPMERDRGAAHSLEPGKENLPG 205
      :   ||| | :| ||:| ||||| |   | :   : |   :| :   |||
Db      146 NHHGGVCRSKSMKLVLRVGQSPDTDSFSAKNHPTRNPPKYPENKDQNTF-----SKENDVS 200
Qy      206 --DPTSNAISRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCW-----RR 253
      |   |   | | | |   | :||   |   | | | :| :
Db      201 QIDSMQNGESGGKSG-----ESVGSAGSDVALFAGV--ASGAVIFILIIIALVALLH 250
Qy      254 RRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEK 313
      || :   :: |   | | | |   :|| ::   :| | :   :||| | |
Db      251 RRHQKHSACQCSGQLPLNTLPKRGS GASGGSNNGSEPSDIIFPIRTSGSM---YCPHYEK 307
Qy      314 VSGDYGHPVYIVQDGPPQSPNNIYY 338
      ||||| ||||| | : ||| :| ||| |
Db      308 VSGDYGHPVYIVQEMPPQNPNANIYY 332

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# RESULT 6

Q9W6H9

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ID   Q9W6H9          PRELIMINARY;      PRT;   205 AA.
AC   Q9W6H9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin-B2 (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97411149; PubMed=9259557;
RA   Smith A., Robinson V., Patel K., Wilkinson D.G.;
RT   "The EphA4 and EphB1 receptor tyrosine kinases and ephrin-B2 ligand
RT   regulate targeted migration of branchial neural crest cells.";
RL   Curr. Biol. 7:561-570(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20099673;
RA   Helbling P.M., Saulnier D.M., Robinson V., Christiansen J.H.,
RA   Wilkinson D.G., Brandli A.W.;
RT   "Comparative analysis of embryonic gene expression defines potential
RT   interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
RL   Dev. Dyn. 216:361-373(1999).
DR   EMBL; AF128844; AAD32610.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
FT   NON_TER      1      1
SQ   SEQUENCE      205 AA;  22256 MW;  7DEDD34277260C87 CRC64;

```

Query Match 13.5%; Score 331; DB 13; Length 205;  
 Best Local Similarity 36.4%; Pred. No. 1.7e-18;  
 Matches 82; Conservative 35; Mismatches 72; Indels 36; Gaps 7;

```

QY      128 EFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSP-----RGGAVPRKPVS 182
      ||: |||||:|:|: ||::: ||||:|: ||:|:| || | ||: |:|
Db      1 EFQRDKDYIIISTSNGLSLEGVNDQEGGVCVTKAMKILMKVGQDPNFHNHRGASSTRRPDH 60

QY      183 EMPM--ERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      | : : | | : | : : | : | | || | : :
Db      61 ESGTNGKSSTTSPHVNGPEGSSTEGKNAGHSSILGSEVAL-----FAGIASGSIIIFIV 113

QY      241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLG-----GGGGMGPREAEPGEL 293
      : : ||| : : | : | | | : || :
Db      114 IIITLVVLLKYYRRRHRKHSPQHT-----TSLSLSTLATPKRSGNNNG---SEPSDI 161

QY      294 GIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
      | || | : ||||| ||||| ||||| : |||| ||||
Db      162 IIPLR---TAEGVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIIY 203
  
```

RESULT 7

Q9U3M2

```

ID   Q9U3M2          PRELIMINARY;          PRT;    237 AA.
AC   Q9U3M2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   C43F9.8 protein.
GN   C43F9.8.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mortimore B.J.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z82262; CAB54195.1; -.
DR   PIR; T19914; T19914.
DR   WormPep; C43F9.8; CE23593.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
SQ   SEQUENCE    237 AA;  26748 MW;  B9B2D9FCC71FE4FC CRC64;
  
```

Query Match 8.8%; Score 214.5; DB 5; Length 237;

Best Local Similarity 25.7%; Pred. No. 3.7e-09;  
Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps 6;

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QY      11 VRVGALLLLGVLGLVS-GLSLEPVYWNSANKRFQAEG-GYVLYPQIGDRLDLLCPRARPP 68
      ::: :|| : : : | |:| | :|: |||: : ||::
Db      1 MQIATFILLSLFPFIGWARKIPDINWISSNPIFDVSNSTDHVISVHIGDRVSIRCPKSD 60

QY      69 GPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQEYSPNLWGHE 128
      |      ||: :||: : | | | : || : : | | |
Db      61 G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE 114

QY      129 FRSHHDYIIA-----TSDGTREGLESQGQVCLTRGMKVLLRVGQ 169
      |: :|::|: |||| ||:: : |:| : ||: |||
Db      115 FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKKDGLCTAKQMKIKFEV 174

QY      170 SPRGGAVPRKPVSEMPMERDRGAAHS 195
      || | : : :::|| | |
Db      175 DRGNIENPK--FAARTLKKDRDAHS 198

```

# RESULT 8

Q9U474

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ID   Q9U474          PRELIMINARY;          PRT;    279 AA.
AC   Q9U474;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VAB-2 (Hypothetical protein Y37E11AR.6).
GN   VAB-2 OR Y37E11AR.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=N2;
RX   MEDLINE=20084449; PubMed=10619431;
RA   Chin-Sang I.D., George S.E., Ding M., Moseley S.L., Lynch A.S.,
RA   Chisholm A.D.;
RT   "The ephrin VAB-2/EFN-1 functions in neuronal signaling to regulate
RT   epidermal morphogenesis in C. elegans.";
RL   Cell 99:781-790(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Miller N., Maggi L.;
RT   "The sequence of C. elegans cosmid Y37E11AR.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN   [4]

```

RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RT "Direct Submission.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF201079; AAF25647.1; -.  
 DR EMBL; AC024759; AAK68436.1; -.  
 DR WormPep; Y37E11AR.6; CE27606.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 SQ SEQUENCE 279 AA; 32068 MW; 8C291A92D97D39EF CRC64;

Query Match 8.1%; Score 198.5; DB 5; Length 279;  
 Best Local Similarity 27.8%; Pred. No. 8.4e-08;  
 Matches 64; Conservative 35; Mismatches 90; Indels 41; Gaps 8;

QY 1 MGPPHSGPGGVRVGALLLLGVLGLV--SGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRL 58  
 | | | : : : | | | : | | | : | | | : | | | | : | | | |  
 Db 1 MHPP-----IKIQTILLF-ILTTVHCSAKRLPQIYWNSTNPLVER-----YAAIGDTL 47  
 QY 59 DLLCPRARPPGPHSSPENYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDPDLDLRFTIKFQ 118  
 | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |  
 Db 48 DIVCPFF---DENSDDELTEQSIIYRVTEEEYENCERRSKAKELGRCTQPYQEEKLKVAFR 104  
 QY 119 EYSPNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPR 178  
 | | | | : : | | | | : : | | : : | | : : | | : : | | : : | | : : | |  
 Db 105 LMSPNPSGLDYRPGVTTYFYFISTSTGSRKGLYNEQGGLCASHNLKMMVIHI--TDRNG---- 158  
 QY 179 KPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAV 228  
 | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
 Db 159 -----DIGPHHHRHHHKKTTTTTTTTSTSTS-----TPKTIPPV 191

# RESULT 9

Q9V4E1

ID Q9V4E1 PRELIMINARY; PRT; 652 AA.  
 AC Q9V4E1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Ephrin protein (LD11109p).  
 GN EPHRIN OR CG1862 OR DSIM\EPHRIN;EPHRIN.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Dai Y., Kunes S.;  
 RT "Isolation and Characterization of Drosophila Ephrin.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanenvong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF216287; AAF28394.1; -.  
 DR EMBL; AE003843; AAF59335.2; -.  
 DR EMBL; BT005199; AAO61756.1; -.  
 DR FlyBase; FBgn0040324; Ephrin.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008972; Cupredoxin.

DR InterPro; IPR001799; Ephrin.  
DR Pfam; PF00812; Ephrin; 1.  
DR PRINTS; PR01347; EPHRIN.  
DR ProDom; PD002533; Ephrin; 1.  
SQ SEQUENCE 652 AA; 72302 MW; 5BA2F02F15964594 CRC64;

Query Match 7.8%; Score 192; DB 5; Length 652;  
Best Local Similarity 21.2%; Pred. No. 7.7e-07;  
Matches 103; Conservative 64; Mismatches 154; Indels 164; Gaps 22;

QY 33 VYWSANKRFQAEG-GYVLYPQIG-----DRLDLLCPRARPPGPHSSPNYEFYKLYLVG 85  
::||::| | : : :: | | : : || | : | |  
Db 219 MHWNTSNSIFRIDNTDHIIDVKNKGNLAFEDQVHIICP-VYEPGTFFENET-EKYIYNVS 276  
  
QY 86 GAQGRRCCEAPPA-PNLLLTCDRDLRLRFITKFEYSPNLWGHEFRSHHDYIIATSDGT 144  
: | | : : ||:| : ||| | : :| | | :||| | :| :  
Db 277 KVEYETCRITNADPRVIAICDKPQKLMFFTTITFRPFTPQPGGLEFLPGNDYYFISTS--S 334  
  
QY 145 REGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSL-----EPG 199  
:: | || | ||| : : | : | | | : : :  
Db 335 KDDLYRRIGGRCSNMMKVVFVCCAPEDNN-KTTALSNSKSVTDTGGAINVNIANNDES 393  
  
QY 200 KENLPGDPTSNATSRGAEG-----PLPP-----P 223  
| : : | : | | : | |  
Db 394 HVNSHGNNAIGTNIGINGGGQIIGGPQSAGIPINPLSGNNNINGIPTTINSNIDQFNRI 453  
  
QY 224 SMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSERHPGPG-SFGRGGSGLGLGGGGG 282  
| : | | : | : || : | | | |  
Db 454 IQPNIIGNHVGTNAVGTGIVGGGGIIL-----TPGHAHGNINMLQPGRGGI 499  
  
QY 283 MGPRAEAPG----ELGIALRG-----GGAADPPFCPHYEKVSGDYGH 320  
| | || : || : | | | | |  
Db 500 NG---AYPGHHHIQTGIRINNVTQHNYPSHKGNANSNINGNDDH---HHYNK-----H 547  
  
QY 321 PVYIVQD-----GPPQSPPNIYYTSISVLEWPILHTIQLFFMRSKCSRVTTFLEFPVQV 373  
| : : : | | || : | : | : || :  
Db 548 PNEVVKNEELTYNSGAATSDGNIFALWIWILS-----IFP--L 583  
  
QY 374 ITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCWFWDRLGTALFVLVLILLGLRLNM 433  
: : | : : : | : | : : | : | :  
Db 584 LSIQSCHLSSY-----WI-----SASFLVSTIALILGIHYL 613  
  
QY 434 HQTTL 438  
| |  
Db 614 IQITL 618

# RESULT 10

Q98TZ1

ID Q98TZ1 PRELIMINARY; PRT; 202 AA.  
AC Q98TZ1;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Ephrin-A6 (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Menzel P., Valencia F., Godement P., Dodelet V.C., Pasquale E.B.;  
 RT "Ephrin-A6, a new ligand for EphA receptors in the developing visual  
 RT system.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF317286; AAK00944.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 202 AA; 22624 MW; 91E2716FF91353F9 CRC64;

Query Match 7.3%; Score 178.5; DB 13; Length 202;  
 Best Local Similarity 27.5%; Pred. No. 2.2e-06;  
 Matches 56; Conservative 27; Mismatches 84; Indels 37; Gaps 7;

Qy 33 VYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRRC 92  
 |||| :| || : | : | | ||: || | | : | :| | |  
 Db 25 VYWNGSNPRF-LQDDYSIQVSINDHLDIYCPHYSAPTPWA----ESFTLFMVDEEGYRGC 79  
 Qy 93 EAPPAPNLLLTCDR---PDLDLRFITIKFQEYSPNLWGHEFRSHHDYIIAT-SDGTREGL 148  
 | | :| : | : ||: | | :| | || | | | : : | :  
 Db 80 SETPGAFKRWECNKPFAPFVPVRFSEKIQRFTPFSLGFEFRPGETYYYISVPTPGS---- 135  
 Qy 149 ESLQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPT 208  
 | || : | | | :| :| :| :| : | | | |  
 Db 136 ----AGRCLKL RVSVCCR-----ASTPEPLTEVPNSQPRGR-----GGPE 171  
 Qy 209 SNATSRGAEGPLPPPSMPAVAGAA 232  
 :| | | :| | : | |  
 Db 172 GDAGSPRDAAPIPQRSRTLRVALA 195

# RESULT 11

Q8N578

ID Q8N578 PRELIMINARY; PRT; 205 AA.  
 AC Q8N578;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Ephrin-A1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Strausberg R.;



RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK009144; BAB26102.1; -.  
 DR MGD; MGI:103236; Efnal.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR InterPro; IPR001680; WD40.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; 1.  
 SQ SEQUENCE 205 AA; 23772 MW; E37E55767459A4EC CRC64;

Query Match 6.8%; Score 167; DB 11; Length 205;  
 Best Local Similarity 26.1%; Pred. No. 1.9e-05;  
 Matches 43; Conservative 34; Mismatches 76; Indels 12; Gaps 4;

QY 18 LLGVLGLVSGLSLEPVYWN SANKRFQ AEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYE 77  
 |||: :: |::|:| ::| |::|:| ||::|| : |  
 Db 8 LLGLCCSLAAADRHIVFWNSSNPKFREE-DYTVHVQLNDYLDIICPHYEDDSV-ADAAME 65  
 QY 78 FYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHD 134  
 | ||:| : |: : |::| : ::||| ::| : | ||: |  
 Db 66 RYTLYMVEHQEYVACQPQSKDQVRWNCNRPSAKHGPEKLSVKFQRFPTFILGKEFKEGHS 125  
 QY 135 YYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179  
 || |: :| || :| ::|:| ::|  
 Db 126 YYYISKPIYHQE-----SQCLKLVTVNGKITHNPQAHVNPQE 163

# RESULT 13

Q9CZS8

ID Q9CZS8 PRELIMINARY; PRT; 206 AA.  
 AC Q9CZS8;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE 10 days embryo cDNA, RIKEN full-length enriched library,  
 DE clone:2610529M21, full insert sequence.  
 GN EFNA4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK012195; BAB28092.1; -.  
 DR MGD; MGI:106643; Efna4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 SQ SEQUENCE 206 AA; 22859 MW; 675E32971D1C6EBC CRC64;

Query Match 6.7%; Score 163.5; DB 11; Length 206;  
 Best Local Similarity 28.1%; Pred. No. 3.6e-05;  
 Matches 61; Conservative 17; Mismatches 80; Indels 59; Gaps 10;

QY 32 PVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRR 91  
 |:||||:| | | | : | ||: || || | | : ||:| :  
 Db 29 PIYWNSSNPRL-LRGDAVVELGFNDYLDIFCPHYESPGPPEGP--ETFALYIVDWSGYEA 85  
 QY 92 CEAPPAPNL-LLTCDRPDL---DLRFITIKFQEYSPNLWGHEFRSHHDYIIATSDGTREG 147  
 | | | : | | : ||: | | | : | | | | | : |  
 Db 86 CTAEGANSFQRWNC SMPFAPFSPVRFSEKIQRYPFPLGFEFLPGETYYYYISVPTPESPG 145  
 QY 148 -LESLQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGA AH-SLEPGKENLPG 205  
 || || : : ||:| | | |  
 Db 146 RCLRLQVSVCC-----KESGSSHESAHP-----VG 170  
 QY 206 DPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240  
 | : || || | | | ||||  
 Db 171 SPGESGTSGWRGGHAPSP-----LCLLLL 194

Q9N178

Query Match 6.3%; Score 155.5; DB 6; Length 675;  
Best Local Similarity 28.5%; Pred. No. 0.00064;  
Matches 103; Conservative 17; Mismatches 113; Indels 129; Gaps 25;

QY	1	MGPPHSGPGGVRVGALLLLGLVLGLVSGLSLEPVYWN	SANKRFQAEGGYVLYPQI-GDR-L	58
			:	
Db	212	MGPP--GPPGV-----	GKR--GENGFPGQPGIKGDRGF	240
QY	59	DLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRR-CEAPPAPNLLTCDRPDLDLRFTIKF		117
			:	
Db	241	PGESGPAGPPGPQGPP-----	GEQGREGIGKPGAPG---AAGQPGL-----	278
QY	118	QEYSPNLWGHEFRSHHDYIIATSDGT----	REGLESLQGGVCLTRGMKVLLRVGQSPRG	173
		:   :    :		
Db	279	----PGTKGHFGAPG----	MAGPPGAPGFGKPGPLPGLKG----QRG-----PIG	315
QY	174	GAVPRKPVSEMPMERDRG-AAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAA		232
		:     : : :	:	
Db	316	--LPGAPGA----	KGEQGPAGHPGEPGLTGPPG-----SRGPQGPKGIPGNNGVPGPK	362
QY	233	GGLALLLLGVAGAGGAMCWRRRR---AKPSES	SRHPG-----PGSFGRGGSGLGLGGGGG	282

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      | : | | | | | | | | | | | | | | | | | | | |
Db      363 GEIG--LAGPAGFPAGKGERGPSGLDGKPGYPGEPGLNGPKGNPGLPGPKGDPGIGGPPG 420
QY      283 M----GPRAE--PGELGIA-LRGG-----GAADPPFCPHYEKVSGDYGHVPYIVQDG 328
      : | | | : | | | | | | | | | | | | | | | |
Db      421 LPGPVGPAGAKGVPGHNGEAGPRGAPGIPGTRGPIGPPGIPGFPGSKGDPGNP-----G 474
QY      329 PP 330
      | |
Db      475 PP 476

```

RESULT 15

O93431

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ID      O93431          PRELIMINARY;          PRT;    229 AA.
AC      O93431;
DT      01-NOV-1998 (TrEMBLrel. 08, Created)
DT      01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Ephrin A-L1.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Durbin L., Brennan C.H., Shiomi K., Cooke J.;
RT      "Eph signalling is required for segmentation and differentiation of
RT      the somites.";
RL      Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AJ006838; CAA07264.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008972; Cupredoxin.
DR      InterPro; IPR001799; Ephrin.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00812; Ephrin; 1.
DR      PRINTS; PR01347; EPHRIN.
DR      ProDom; PD002533; Ephrin; 1.
DR      PROSITE; PS01299; EPHRIN; 1.
DR      PROSITE; PS00290; IG_MHC; 1.
SQ      SEQUENCE    229 AA;  26115 MW;  8684462F67AF6F5C CRC64;

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Query Match          6.3%; Score 155; DB 13; Length 229;
Best Local Similarity 27.2%; Pred. No. 0.00019;
Matches 56; Conservative 23; Mismatches 93; Indels 34; Gaps 7;

```

```

QY      33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC 92
      | | | | | | : | : : | | | : | | | | | | | |
Db      25 VYWNSTNANFLWD-DYTVDVIRINDYLDIICPH-YAHGEIASQEAERYVLYMVELEDYENC 82
QY      93 EAPPAPNLLLTCDR---PDLDLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGTREGLE 149
      : | | | | : | : | | : | | | | | | :
Db      83 KPHSFDQLRWECSRPFAPHAPEKFSEKFQRFPTFTLGKEFRQGESYYYIS-----K 133
QY      150 SL--QGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDP 207
      | | | | : | : | | : | : : | | : | |

```

Db 134 PLHHHGQECLRLKVDVV-----GPHGSKNKKKMVEKVEEIEGKMAAGGVHNP SNRLPADD 188  
QY 208 TSNATSRGAEGPLPPPSMPAVAGAAG 233  
| :| | :|  
Db 189 -----PIAMIPVVQRSVG 201

Search completed: September 15, 2004, 12:39:12  
Job time : 91.1384 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:22:15 ; Search time 17.7421 Seconds  
(without alignments)  
1335.348 Million cell updates/sec

Title: US-10-021-121-2  
Perfect score: 2450  
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1841	75.1	340	1	EFB3_HUMAN	Q15768 homo sapien
2	1771	72.3	340	1	EFB3_MOUSE	O35393 mus musculu
3	628.5	25.7	336	1	EFB2_MOUSE	P52800 mus musculu
4	623	25.4	346	1	EFB1_HUMAN	P98172 homo sapien
5	620.5	25.3	333	1	EFB2_HUMAN	P52799 homo sapien
6	619	25.3	334	1	EFB1_CHICK	O73612 gallus gall
7	617.5	25.2	332	1	EFB2_BRARE	O73874 brachydanio
8	604.5	24.7	345	1	EFB1_MOUSE	P52795 mus musculu
9	599.5	24.5	345	1	EFB1_RAT	P52796 rattus norv
10	591	24.1	327	1	EFB1_XENLA	O13097 xenopus lae
11	185	7.6	195	1	EFA2_BRARE	P79727 brachydanio
12	179	7.3	238	1	EFA3_HUMAN	P52797 homo sapien
13	176	7.2	209	1	EFA2_MOUSE	P52801 mus musculu
14	175.5	7.2	213	1	EFA2_HUMAN	O43921 homo sapien
15	172	7.0	200	1	EFA2_CHICK	P52802 gallus gall
16	170.5	7.0	228	1	EFA5_CHICK	P52804 gallus gall
17	169.5	6.9	201	1	EFA4_HUMAN	P52798 homo sapien



18	169.5	6.9	228	1	EFA5_BRARE	P79728	brachydanio
19	167.5	6.8	216	1	EFA1_XENLA	P52794	xenopus lae
20	167.5	6.8	228	1	EFA5_HUMAN	P52803	homo sapien
21	167.5	6.8	228	1	EFA5_MOUSE	O08543	mus musculu
22	167.5	6.8	228	1	EFA5_RAT	P97605	rattus norv
23	166	6.8	205	1	EFA1_HUMAN	P20827	homo sapien
24	162.5	6.6	205	1	EFA1_RAT	P97553	rattus norv
25	161	6.6	205	1	EFA1_MOUSE	P52793	mus musculu
26	160.5	6.6	206	1	EFA4_MOUSE	O08542	mus musculu
27	159	6.5	680	1	CA1A_MOUSE	Q05306	mus musculu
28	154.5	6.3	1049	1	CA13_BOVIN	P04258	bos taurus
29	151.5	6.2	301	1	CC02_CAEEL	P17656	caenorhabdi
30	148.5	6.1	1670	1	CA34_HUMAN	Q01955	homo sapien
31	146.5	6.0	1774	1	CA1H_MOUSE	P39061	mus musculu
32	146	6.0	1027	1	CAFF_RIFPA	P30754	riftia pach
33	145	5.9	674	1	CA1A_BOVIN	P23206	bos taurus
34	145	5.9	1745	1	CA35_HUMAN	P25940	homo sapien
35	144.5	5.9	1516	1	CA1H_HUMAN	P39060	homo sapien
36	144	5.9	675	1	CA39_CHICK	P32017	gallus gall
37	144	5.9	921	1	CA19_HUMAN	P20849	homo sapien
38	143	5.8	674	1	CA1A_CHICK	P08125	gallus gall
39	142.5	5.8	635	1	CA28_HUMAN	P25067	homo sapien
40	142.5	5.8	1496	1	CA25_HUMAN	P05997	homo sapien
41	142	5.8	744	1	CA18_HUMAN	P27658	homo sapien
42	142	5.8	1029	1	CA26_MOUSE	Q02788	mus musculu
43	142	5.8	1763	1	CA24_ASCSU	P27393	ascaris suu
44	141.5	5.8	1466	1	CA13_HUMAN	P02461	homo sapien
45	141	5.8	744	1	CA18_RABIT	P14282	oryctolagus

# ALIGNMENTS

## RESULT 1

### EFB3\_HUMAN

ID EFB3\_HUMAN STANDARD; PRT; 340 AA.  
AC Q15768; O00680; Q8TBH7; Q92875;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ephrin-B3 precursor (EPH-related receptor tyrosine kinase ligand 8)  
DE (LERK-8) (EPH-related receptor transmembrane ligand ELK-L3).  
GN EFNB3 OR EPLG8 OR LERK8.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cerretti D.P.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=97271551; PubMed=9126477;  
RA Tang X.X., Pleasure D.E., Ikegaki N.;  
RT "cdNA cloning, chromosomal localization, and expression pattern of

RT EPLG8, a new member of the EPLG gene family encoding ligands of EPH-  
 RT related protein-tyrosine kinase receptors.";  
 RL Genomics 41:17-24(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain cortex;  
 RX MEDLINE=96404527; PubMed=8808709;  
 RA Gale N.W., Flenniken A., Compton D.C., Jenkins N.A., Copeland N.G.,  
 RA Gilbert D.J., Davis S., Wilkinson D.G., Yancopoulos G.D.;  
 RT "Elk-L3, a novel transmembrane ligand for the Eph family of receptor  
 RT tyrosine kinases, expressed in embryonic floor plate, roof plate and  
 RT hindbrain segments.";  
 RL Oncogene 13:1343-1352(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,  
 CC and induce the collapse of, commissural axons/growth cones in  
 CC vitro. May play a role in constraining the orientation of  
 CC longitudinally projecting axons (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain; expressed in  
 CC embryonic floor plate, roof plate and hindbrain segments.  
 CC -!- SIMILARITY: Belongs to the ephrin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U57001; AAB05170.1; -.  
 DR EMBL; U66406; AAC51203.1; -.  
 DR EMBL; U62775; AAC50707.1; -.

DR EMBL; BC022499; AAH22499.1; -.  
 DR EMBL; BC042944; AAH42944.1; -.  
 DR Genew; HGNC:3228; EFNB3.  
 DR MIM; 602297; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0007399; P:neurogenesis; TAS.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;  
 KW Signal; Polymorphism.  
 FT SIGNAL 1 27 POTENTIAL.  
 FT CHAIN 28 340 EPHRIN-B3.  
 FT DOMAIN 28 226 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 227 247 POTENTIAL.  
 FT DOMAIN 248 340 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 338 340 PDZ RECOGNITION MOTIF (POTENTIAL).  
 FT DISULFID 62 104 BY SIMILARITY.  
 FT DISULFID 92 156 BY SIMILARITY.  
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 166 166 R -> Q.  
 FT /FTId=VAR\_002356.  
 SQ SEQUENCE 340 AA; 35834 MW; EDFF2A23C2FDE79F CRC64;

Query Match 75.1%; Score 1841; DB 1; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 1e-113;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Qy	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Qy	241	GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Qy	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY	338
Db	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY	338

# RESULT 2

## EFB3\_MOUSE

ID EFB3\_MOUSE STANDARD; PRT; 340 AA.  
AC O35393;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ephrin-B3 precursor.  
GN EFNB3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98143367; PubMed=9484836;  
RA Bergemann A.D., Zhang L., Chiang M.-K., Brambilla R., Klein R.,  
RA Flanagan J.G.;  
RT "Ephrin-B3, a ligand for the receptor EphB3, expressed at the midline  
RT of the developing neural tube.";  
RL Oncogene 16:471-480(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP FUNCTION.  
RX MEDLINE=20171264; PubMed=10704386;  
RA Imondi R., Wideman C., Kaprielian Z.;  
RT "Complementary expression of transmembrane ephrins and their receptors  
RT in the mouse spinal cord: a possible role in constraining the  
RT orientation of longitudinally projecting axons.";  
RL Development 127:1397-1410(2000).  
CC -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,  
CC and induce the collapse of, commissural axons/growth cones in

```

CC      vitro. May play a role in constraining the orientation of
CC      longitudinally projecting axons.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
CC      specifically on commissural axon segments that have passed through
CC      the floor plate. Expressed in cells of the retinal ganglion cell
CC      layer during retinal axon guidance to the optic disk.
CC      -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
CC      period of commissural axon pathfinding.
CC      -!- SIMILARITY: Belongs to the ephrin family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF025288; AAC53537.1; -.
DR      EMBL; BC052001; AAH52001.1; -.
DR      EMBL; BC058617; AAH58617.1; -.
DR      MGD; MGI:109196; Efnb3.
DR      GO; GO:0007628; P:adult walking behavior; IMP.
DR      GO; GO:0007411; P:axon guidance; IMP.
DR      InterPro; IPR008972; Cupredoxin.
DR      InterPro; IPR001799; Ephrin.
DR      Pfam; PF00812; Ephrin; 1.
DR      PRINTS; PR01347; EPHRIN.
DR      ProDom; PD002533; Ephrin; 1.
DR      PROSITE; PS01299; EPHRIN; 1.
KW      Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW      Signal.
FT      SIGNAL          1      27      POTENTIAL.
FT      CHAIN           28     340     EPHRIN-B3.
FT      DOMAIN          28     227     EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        228     248     POTENTIAL.
FT      DOMAIN          249     340     CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          338     340     PDZ RECOGNITION MOTIF (POTENTIAL).
FT      DISULFID         62     104     BY SIMILARITY.
FT      DISULFID         92     156     BY SIMILARITY.
FT      CARBOHYD        210     210     N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE      340 AA;  35884 MW;  52F3D58FD209A6B8 CRC64;

Query Match          72.3%; Score 1771; DB 1; Length 340;
Best Local Similarity 95.6%; Pred. No. 3.9e-109;
Matches 323; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY      1 MGPPHSGPGGVVRGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
      || || |||||:||||||| |||||
Db      1 MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

QY      61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
      |||||:||||||| |||||
Db      61 LCPRARPPGPHSSPSYEFYKLYLVEGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

QY      121 SPNLWGHEFRSHHDYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

```



RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP FUNCTION.  
 RX MEDLINE=20171264; PubMed=10704386;  
 RA Imondi R., Wideman C., Kaprielian Z.;  
 RT "Complementary expression of transmembrane ephrins and their receptors  
 RT in the mouse spinal cord: a possible role in constraining the  
 RT orientation of longitudinally projecting axons.";  
 RL Development 127:1397-1410(2000).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (1.92 ANGSTROMS) OF 30-170.  
 RX MEDLINE=21563306; PubMed=11703926;  
 RA Toth J., Cutforth T., Gelinas A.D., Bethoney K.A., Bard J.,  
 RA Harrison C.J.;  
 RT "Crystal structure of an ephrin ectodomain.";  
 RL Dev. Cell 1:83-92(2001).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 31-168 IN COMPLEX WITH  
 RP EPHB2.  
 RX MEDLINE=21638766; PubMed=11780069;  
 RA Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A.,  
 RA Henkemeyer M., Nikolov D.B.;  
 RT "Crystal structure of an Eph receptor-ephrin complex.";  
 RL Nature 414:933-938(2001).  
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB2 and EPHB4.  
 CC May play a role in constraining the orientation of longitudinally  
 CC projecting axons.  
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,  
 CC specifically on commissural axon segments that have passed through  
 CC the floor plate. Expressed in cells of the retinal ganglion cell  
 CC layer during retinal axon guidance to the optic disk.  
 CC -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the

CC period of commissural axon pathfinding.  
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the  
 CC cytoplasmic domain (By similarity).  
 CC -!- SIMILARITY: Belongs to the ephrin family.  
 CC -----  
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 CC -----  
 DR EMBL; U16819; AAA99708.1; -.  
 DR EMBL; L38847; AAC42052.1; -.  
 DR EMBL; U30244; AAA82934.1; -.  
 DR EMBL; BC057009; AAH57009.1; -.  
 DR PIR; I49766; I49766.  
 DR PDB; 1IKO; 15-MAY-02.  
 DR PDB; 1KGY; 28-MAY-02.  
 DR MGD; MGI:105097; Efnb2.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;  
 KW Signal; Phosphorylation; 3D-structure.  
 FT SIGNAL 1 28 POTENTIAL.  
 FT CHAIN 29 336 EPHRIN-B2.  
 FT DOMAIN 29 232 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 233 253 POTENTIAL.  
 FT DOMAIN 254 336 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 334 336 PDZ RECOGNITION MOTIF (POTENTIAL).  
 FT DISULFID 65 104  
 FT DISULFID 92 156  
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 3 4 MISSING (IN REF. 3).  
 FT CONFLICT 177 177 A -> T (IN REF. 1).  
 SQ SEQUENCE 336 AA; 37202 MW; D08894996E399554 CRC64;

Query Match 25.7%; Score 628.5; DB 1; Length 336;  
 Best Local Similarity 41.8%; Pred. No. 2.3e-34;  
 Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDLLCPRARPPGPHSS 73  
 | |::| : : |||:||||:| :| | |||||:|::|: :  
 Db 17 GLLMVLCRTAISRSIVLEPIYWSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73  
 Qy 74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133  
 ||::|:|:| | || || | ||| :::|:|||||:|:| ||: :  
 Db 74 GQYEYYKVYMVVDKQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133  
 Qy 134 DYYIIATSDGTREGLESQGGLVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190  
 ||||:|:|:| ||:: :||| || ||:|:|:| | | | :|



Db 134 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

QY 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250  
| : : | : || | : : | : || | : : : :

Db 194 GRSSTTSPFVKPNPGSSTDGNSAGHSNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

QY 251 WRRRRRAKPSESRHPGPGSFGRRGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310  
||| : : | : | : || : || : | || || |||

Db 254 KYRRRHRKHSPQHTTTTSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

QY 311 YEKVSGDYGHPVYIVQDGPQSPNIIY 338  
||||||| : |||| |||

Db 307 YEKVSGDYGHPVYIVQEMPQSPANIIY 334

#### RESULT 4

##### EFB1\_HUMAN

ID EFB1\_HUMAN STANDARD; PRT; 346 AA.

AC P98172;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)

DE (LERK-2) (ELK ligand) (ELK-L).

GN EFNBI OR EPLG2 OR LERK2 OR EFL-3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=94349923; PubMed=8070404;

RA Beckmann M.P., Cerretti D.P., Baum P., Vanden Bos T., James L.,

RA Farrah T., Kozlosky C., Hollingsworth T., Shilling H., Maraskovsky E.,

RA Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;

RT "Molecular characterization of a family of ligands for eph-related

RT tyrosine kinase receptors.";

RL EMBO J. 13:3757-3762(1994).

RN [2]

RP SEQUENCE FROM N.A.

RA Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V.,

RA Pawson T., Goldfarb M., Yancopoulos G.D.;

RL Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Fletcher F.A., Huebner K., Shaffer L.G., Monaco A., Mueller U.,

RA Kozlosky C., Druck T., Simoneaux D.K., Fairweather N., Chelly J.,

RA Cerretti D.P., Belmont J.W., Beckmann M.P., Lyman S.D.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Howden P.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Eye, and Skin;

RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and EPHA1.  
 CC Binds to, and induce the collapse of, commissural axons/growth  
 CC cones in vitro. May play a role in constraining the orientation of  
 CC longitudinally projecting axons (By similarity).  
 CC -!- SUBUNIT: Binds GRIP1 and GRIP2.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Heart, placenta, lung, liver, skeletal muscle,  
 CC kidney, pancreas.  
 CC -!- INDUCTION: By TNF-alpha.  
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the  
 CC cytoplasmic domain (By similarity).  
 CC -!- SIMILARITY: Belongs to the ephrin family.  
 CC -----  
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 CC -----  
 DR EMBL; U09304; AAA53093.1; -.  
 DR EMBL; L37361; AAA52369.1; -.  
 DR EMBL; U09303; AAB41127.1; -.  
 DR EMBL; AL136032; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; BC016649; AAH16649.1; -.  
 DR EMBL; BC052979; AAH52979.1; -.  
 DR PIR; S46993; S46993.  
 DR Genew; HGNC:3226; EFNBL1.  
 DR MIM; 300035; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0005108; F:transmembrane ephrin; TAS.  
 DR GO; GO:0007155; P:cell adhesion; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR InterPro; IPR008972; Cupredoxin.

DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;  
 KW Signal; Phosphorylation.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 346 EPHRIN-B1.  
 FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 238 258 POTENTIAL.  
 FT DOMAIN 259 346 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 344 346 PDZ RECOGNITION MOTIF (POTENTIAL).  
 FT DISULFID 64 101 BY SIMILARITY.  
 FT DISULFID 89 153 BY SIMILARITY.  
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 346 AA; 38006 MW; 473DD2F1A5BF89DE CRC64;

Query Match 25.4%; Score 623; DB 1; Length 346;  
 Best Local Similarity 39.2%; Pred. No. 5.4e-34;  
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy 8 PGGVRVGGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 61  
 || :| |: |: : | :||| |:| |:| :| :| |:|:| |:|:|  
 Db 4 PGQRWLKGKLVAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63  
 Qy 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQEYS 121  
 |||| | :|:|:| | | :|:|:|:|:| :|:|:|:|:|  
 Db 64 CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118  
 Qy 122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181  
 || | |:| |:|:| :|:|:| |:|:| :|:| | | |:|:|:| | :  
 Db 119 PNYMGLEFKKHHDYIITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQLTT 178  
 Qy 182 SEMPMERDRGAHSLE-PGKENLPGDPTSNA TSGAEGPLPPPSMPAVAGAAGGLA---- 236  
 | | | : : || | | : | | | |:|:| :  
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231  
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277  
 : | || | :|:| | :| :| | :| |  
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLL LKLRKRHRKHTQQ-----RAAALSL 282  
 Qy 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333  
 || | || :|:| | : :|:|:|:|:|:|:|:|:|:|:|:|:|  
 Db 283 STLASPKGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339  
 Qy 334 PNIYY 338  
 ||||  
 Db 340 ANIYY 344

# RESULT 5

## EFB2\_HUMAN

ID EFB2\_HUMAN STANDARD; PRT; 333 AA.  
 AC P52799;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)  
 DE (LERK-5) (HTK ligand) (HTK-L).  
 GN EFNB2 OR EPLG5 OR LERK5 OR HTKL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=96145238; PubMed=8559144;  
 RA Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,  
 RA Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,  
 RA Jenkins N.A., Fletcher R.A.;  
 RT "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine  
 RT kinases.";  
 RL Mol. Immunol. 32:1197-1205(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95199254; PubMed=7534404;  
 RA Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,  
 RA Gillett N., Matthews W.;  
 RT "Molecular cloning of a ligand for the EPH-related receptor protein-  
 RT tyrosine kinase Htk.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98192220; PubMed=9533549;  
 RA Vogt T., Stolz W., Welsh J., Jung B., Kerbel R.S., Kobayashi H.,  
 RA Landthaler M., McClelland M.;  
 RT "Overexpression of Lerk-5/Eplg5 messenger RNA: a novel marker for  
 RT increased tumorigenicity and metastatic potential in human malignant  
 RT melanomas.";  
 RL Clin. Cancer Res. 4:791-797(1998).  
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.  
 CC May play a role in constraining the orientation of longitudinally  
 CC projecting axons (By similarity).  
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Lung and kidney.  
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the  
 CC cytoplasmic domain (By similarity).  
 CC -!- SIMILARITY: Belongs to the ephrin family.  
 CC -----  
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 CC -----  
 DR EMBL; U16797; AAA99707.1; -.  
 DR EMBL; L38734; AAC41752.1; -.  
 DR EMBL; U81262; AAD03786.1; -.

DR PIR; I84743; I84743.  
 DR Genew; HGNC:3227; EFNB2.  
 DR MIM; 600527; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005106; F:ephrin; TAS.  
 DR GO; GO:0005108; F:transmembrane ephrin; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;  
 KW Signal; Phosphorylation.  
 FT SIGNAL 1 27 POTENTIAL.  
 FT CHAIN 28 333 EPHRIN-B2.  
 FT DOMAIN 28 229 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 230 250 POTENTIAL.  
 FT DOMAIN 251 333 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 331 333 PDZ RECOGNITION MOTIF (POTENTIAL).  
 FT DISULFID 62 101 BY SIMILARITY.  
 FT DISULFID 89 153 BY SIMILARITY.  
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 333 AA; 36923 MW; 6D9932A632626AEA CRC64;

Query Match 25.3%; Score 620.5; DB 1; Length 333;  
 Best Local Similarity 40.5%; Pred. No. 7.6e-34;  
 Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

Qy 14 GALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73  
 | |::| : : ||:||||:| :| | |||||::|::|: :  
 Db 14 GVLMLCRTAISKSIWLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70  
 Qy 74 PNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133  
 ||:|::|:| | || || | :|| |::| |||||:||||| ||: :  
 Db 71 GQYEYYKVYMVDDKDQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK 130  
 Qy 134 DYYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190  
 ||||:|::|: ||::: :||| || ||:|::||| | | : | :|  
 Db 131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190  
 Qy 191 GAAHSLEPGKENLPGDPTSNAISRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250  
 | : : | : || | : : : : : || | | : : : :  
 Db 191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250  
 Qy 251 WRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310  
 ||| : :| | : | : || :||:| || || |||  
 Db 251 KYRRRRHRKHSPQHTTTLSTLATPKRSGNN---NGSEPSDIIIPLR---TADSVFCPH 303  
 Qy 311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338  
 ||||| |||||: |||| ||||  
 Db 304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331

## RESULT 6

EFB1\_CHICK

ID EFB1\_CHICK STANDARD; PRT; 334 AA.  
AC 073612;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ephrin-B1 precursor (CEK5 ligand) (CEL5-L).  
GN EFNBL.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97223524; PubMed=9070326;  
RA Holash J.A., Soans C., Chong L.D., Shao H., Dixit V.M.,  
RA Pasquale E.B.;  
RT "Reciprocal expression of the Eph receptor Cek5 and its ligand(s) in  
RT the early retina.";  
RL Dev. Biol. 182:256-269(1997).  
CC -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB2.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- PTM: Inducible phosphorylation of tyrosine residues in the  
CC cytoplasmic domain (By similarity).  
CC -!- SIMILARITY: Belongs to the ephrin family.  
CC -----  
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CC -----  
DR EMBL; U72394; AAC07986.1; -.  
DR InterPro; IPR008972; Cupredoxin.  
DR InterPro; IPR001799; Ephrin.  
DR Pfam; PF00812; Ephrin; 1.  
DR PRINTS; PR01347; EPHRIN.  
DR ProDom; PD002533; Ephrin; 1.  
DR PROSITE; PS01299; EPHRIN; 1.  
KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;  
KW Signal; Phosphorylation.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 334 EPHRIN-B1.  
FT DOMAIN 26 231 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 232 252 POTENTIAL.  
FT DOMAIN 253 334 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 332 334 PDZ RECOGNITION MOTIF (POTENTIAL).  
FT DISULFID 60 97 BY SIMILARITY.  
FT DISULFID 85 149 BY SIMILARITY.  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 334 AA; 36858 MW; 48AF556E9ED56CD5 CRC64;

Query Match

25.3%; Score 619; DB 1; Length 334;

Best Local Similarity 39.3%; Pred. No. 9.5e-34;  
Matches 144; Conservative 50; Mismatches 100; Indels 72; Gaps 13;

```

Qy      8 PGGVR--VGALLLLGLVGLVSGLSLEPVYWSANKRFQAEGGYVLYPQIGDRDLDCPRA 65
      | | | :| || | | | |||| |:: | :| : | |::|||:|::|:|:|
Db      4 PRGGRWLLGVLLALCRLAAPLAKSLEPVSWASAGNPKFMSGKGLVIYPEIGDKLDIICPKA 63

Qy     66 RPPGPHSSPNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRFTIKFQEYSPNLW 125
      | | | |::||| | | | |::|||:|::|:|:|:|:|:|:|:|
Db     64 EPSKP-----YDYKLYLVKKDQADACSTVMDPNVLVTCNRPEQEIRFTIKFQEFSPNYM 118

Qy    126 GHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGAVPRKPVSEMP 185
      | ||: ||:| :||:| :||:| :||| || ||:::| | | :| : : |
Db    119 GLEFKRQQDYFITSTSNGLDGLNREGGVCQTRSMKIVMKVGQDP-NAVIPEQLTTSRP 177

Qy    186 MER-----DRGAAHSL----EPGKENLPGDPTSNA--TSRGAEGPLPPPSMPAVAGA 231
      : : | : ||| || | | :| | | || |
Db    178 SKEADNTVKIVTQSPRHKVPTVEEPGK---PGSVNQNGQETQGPSDGFL--SSKVAVFAA 232

Qy    232 AGG-----LALLLLGVAGAGGAMCWRRRRAKPSERH-----PGPGSFGRG 272
      | | | |::: | | | |:: | | |
Db    233 IGAGCVIFILIIIFLVLLIKI-----RKRHRKHTQQRAAALSLSTLASPKCSGNA 283

Qy    273 GSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQS 332
      || | |:: | | | : |||||:|:|:|:|:|:|:|:|
Db    284 GS-----EPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQS 326

Qy    333 PPNIYY 338
      | |||
Db    327 PANIYY 332

```

#### RESULT 7

##### EFB2\_BRARE

```

ID   EFB2_BRARE          STANDARD;          PRT;   332 AA.
AC   073874;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B2 precursor (Ephrin B2a).
GN   EFNB2 OR EFNB2A.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98438455; PubMed=9765210;
RA   Durbin L., Brennan C., Shiomi K., Cooke J., Barrios A.,
RA   Shanmugalingam S., Guthrie B., Lindberg R., Holder N.;
RT   "Eph signaling is required for segmentation and differentiation of
RT   the somites.";
RL   Genes Dev. 12:3096-3109(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;

```

RA Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,  
 RA Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;  
 RT "Morphogenesis of prechordal plate and notochord requires intact  
 RT eph/ephrin b signaling.";  
 RL Dev. Biol. 234:470-482(2001).  
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the  
 CC cytoplasmic domain (By similarity).  
 CC -!- SIMILARITY: Belongs to the ephrin family.  
 CC -----  
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 CC -----  
 DR EMBL; AJ004863; CAA06168.1; -.  
 DR EMBL; AF375225; AAK64275.1; -.  
 DR ZFIN; ZDB-GENE-990415-67; efnb2a.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;  
 KW Signal; Phosphorylation.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 332 EPHRIN-B2.  
 FT DOMAIN 25 225 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 226 246 POTENTIAL.  
 FT DOMAIN 247 332 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 330 332 PDZ RECOGNITION MOTIF (POTENTIAL).  
 FT DISULFID 59 98 BY SIMILARITY.  
 FT DISULFID 86 150 BY SIMILARITY.  
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 332 AA; 36724 MW; 189ED82372C71C8B CRC64;

Query Match 25.2%; Score 617.5; DB 1; Length 332;  
 Best Local Similarity 41.8%; Fred. No. 1.2e-33;  
 Matches 143; Conservative 54; Mismatches 106; Indels 39; Gaps 12;

Qy 14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73  
 | |:: : | | : :||: | : | | | | | : : : | |  
 Db 11 GVLVIACKVNLSRALILDSIYWNTTNTKFPVPGQGLVLYPQIGDKMDIVCPVE---GGSM 67  
 Qy 74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133  
 | : | | | : | : | : | | : | | : : | | | | | | | |  
 Db 68 EGVEYYKLYMVPLEQLKSCQVTKADTPLLNCVKPDQDVKFTLKFQEFSPNLWGLEFFRGK 127  
 Qy 134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRK-PVSEMPMERDRGA 192





RL J. Biol. Chem. 269:26606-26609(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP FUNCTION.  
 RX MEDLINE=20171264; PubMed=10704386;  
 RA Imondi R., Wideman C., Kaprielian Z.;  
 RT "Complementary expression of transmembrane ephrins and their receptors  
 RT in the mouse spinal cord: a possible role in constraining the  
 RT orientation of longitudinally projecting axons.";  
 RL Development 127:1397-1410(2000).  
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and EPHA1.  
 CC Binds to, and induce the collapse of, commissural axons/growth  
 CC cones in vitro. May play a role in constraining the orientation of  
 CC longitudinally projecting axons.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,  
 CC specifically on commissural axon segments that have passed through  
 CC the floor plate. Expressed in cells of the retinal ganglion cell  
 CC layer during retinal axon guidance to the optic disc.  
 CC -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the  
 CC period of commissural axon pathfinding.  
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the  
 CC cytoplasmic domain.  
 CC -!- SIMILARITY: Belongs to the ephrin family.  
 CC -----  
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 CC -----  
 DR EMBL; U07602; AAC53247.1; -.



RESULT 9

EFB1\_RAT

ID EFB1\_RAT STANDARD; PRT; 345 AA.  
AC P52796;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)  
DE (LERK-2) (ELK ligand) (ELK-L).  
GN EFNBI OR EPLG2 OR LERK2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=95022634; PubMed=7936648;  
RA Fletcher F.A., Carpenter M., Shilling H., Baum P., Ziegler S.,  
RA Gimpel S., Hollingsworth T., Vanden Bos T., Davison B.L.,  
RA Lyman S.D., Beckmann M.P.;  
RT "LERK-2, a binding protein for the receptor-tyrosine kinase ELK, is  
RT evolutionarily conserved and expressed in a developmentally regulated  
RT pattern.";  
RL Oncogene 9:3241-3248(1994).  
CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB3  
CC (preferred), EPHB1 and EPHA1. Binds to, and induce the collapse  
CC of, commissural axons/growth cones in vitro. May play a role in  
CC constraining the orientation of longitudinally projecting axons  
CC (By similarity).  
CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHB3 (preferred),  
CC EPHB1 and EPHB2.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- PTM: Inducible phosphorylation of tyrosine residues in the  
CC cytoplasmic domain (By similarity).  
CC -!- SIMILARITY: Belongs to the ephrin family.  
CC -----  
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CC -----  
DR EMBL; U07560; AAA53092.1; -.  
DR PIR; I58406; I58406.  
DR InterPro; IPR008972; Cupredoxin.  
DR InterPro; IPR001799; Ephrin.  
DR Pfam; PF00812; Ephrin; 1.  
DR PRINTS; PR01347; EPHRIN.  
DR ProDom; PD002533; Ephrin; 1.  
DR PROSITE; PS01299; EPHRIN; 1.  
KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;  
KW Signal; Phosphorylation.

FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	345	EPHRIN-B1.
FT	DOMAIN	25	236	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	237	257	POTENTIAL.
FT	DOMAIN	258	345	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	343	345	PDZ RECOGNITION MOTIF (POTENTIAL).
FT	DISULFID	64	101	BY SIMILARITY.
FT	DISULFID	89	153	BY SIMILARITY.
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	345 AA;	37951 MW;	1B3045C5C7358F7E CRC64;

Query Match 24.5%; Score 599.5; DB 1; Length 345;  
 Best Local Similarity 37.6%; Pred. No. 1.9e-32;  
 Matches 135; Conservative 52; Mismatches 107; Indels 65; Gaps 10;

Qy	15	ALLLLGVLGLVSGL--SLEPVYWSANKRFQAEGGYVLYPQIGDRDLDCPRARPPGPHS	72
Db	15	AMVVLTLCLATPLAKNLEPVSWSSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP--	72
Qy	73	SPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRDLRFTIKFQEYSPNLWGHEFRSH	132
Db	73	---YEYYKLYLVRPEQAAACSTVLDPNVLVTCKNPQQEIRFTIKFQEFSNYMGLEFKKY	129
Qy	133	HDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGA	192
Db	130	HDYYITSTSNGLSLEGLNREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT	188
Qy	193	AHSLEPGKENLPGDPTSNA TSRGAE GP-----LPPPSMPAVAGAAGG-----LA	236
Db	189	VKT-----ATQAPGRGSQGDSDGKHETVNQQEKGSGPGAGGSGSGDTSFFNSK	236
Qy	237	LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL---GG	279
Db	237	VALFAAVGAGCVIFLLIIIFLTVLLKLRKRHRKHTQQ-----RAAALS LSTLASP	287
Qy	280	GGGMGPRAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYY	338
Db	288	KDGS GTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY	343

# RESULT 10

EFB1\_XENLA

ID EFB1\_XENLA STANDARD; PRT; 327 AA.

AC O13097;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)  
 (LERK-2) (ELK ligand) (ELK-L) (XLERK).

GN EFNBI OR EPLG2 OR LERK2.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

```

RX  MEDLINE=97316777; PubMed=9174051;
RA  Jones T.L., Karavanova I., Chong L., Zhou R.P., Daar I.O.;
RT  "Identification of XLerk, an Eph family ligand regulated during
RT  mesoderm induction and neurogenesis in Xenopus laevis.";
RL  Oncogene 14:2159-2166(1997).
CC  -!- FUNCTION: May have a role in the developing mesenchymal and
CC  nervous tissue.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- TISSUE SPECIFICITY: In the adult, expressed at low levels in most
CC  adult tissues with increased levels observed in the kidney,
CC  oocytes, ovary and testis.
CC  -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC  cytoplasmic domain (By similarity).
CC  -!- SIMILARITY: Belongs to the ephrin family.
CC  -----
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CC  -----
DR  EMBL; U31427; AAC35995.1; -.
DR  InterPro; IPR008972; Cupredoxin.
DR  InterPro; IPR001799; Ephrin.
DR  Pfam; PF00812; Ephrin; 1.
DR  PRINTS; PR01347; EPHRIN.
DR  ProDom; PD002533; Ephrin; 1.
DR  PROSITE; PS01299; EPHRIN; 1.
KW  Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW  Signal; Phosphorylation.
FT  SIGNAL          1      20      POTENTIAL.
FT  CHAIN           21     327     EPHRIN-B1.
FT  DOMAIN          21     225     EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM        226     246     POTENTIAL.
FT  DOMAIN          247     327     CYTOPLASMIC (POTENTIAL).
FT  DOMAIN          325     327     PDZ RECOGNITION MOTIF (POTENTIAL).
FT  DISULFID        57      93     BY SIMILARITY.
FT  DISULFID        81     145     BY SIMILARITY.
FT  CARBOHYD        131     131     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        202     202     N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE        327 AA;  36621 MW;  71230CE7F6BE5974 CRC64;

Query Match          24.1%; Score 591; DB 1; Length 327;
Best Local Similarity 39.5%; Pred. No. 6.3e-32;
Matches 144; Conservative 43; Mismatches 100; Indels 78; Gaps 12;

QY      10 GVR--VGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL DLCPR-- 65
      |:|  :| ||:| |   | :||| ||| | || : | ||||:|||||:|:|:|
Db       3 GLRRLGLLLVLYRLCSALGKNLEPVTWNSQNPRFISGKGLVLYPEIGDRLDIICPKGLF 62

QY      66 RPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDL DLRTIKFQ EYSPNLW 125
      :|  ||:||||:| |   | ||:|:|:| | : |||||:|:|:|
Db      63 QP-----YEYYKLYMVR RDQLEACSTVIDPNVLVTCNQPGKEYRFTIKFQEFSPNYM 114

QY      126 GHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMP 185

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Db      115 GLEFRRNQDYITSTSNSTLQGLNREGGVCQTRSMKIIMKVGQDP--NAVPPPEQLT--- 169
Qy      186 MERDRGAAHSLEPGKENLPGDPTSNATSRGA-EGPLPPP-----SMPAVAGAAGGLA 236
      : | | | | : | | : | : | | : | | | | | | : | | : | |
Db      170 -----TTRPSKE---ADNTGKIATFGPWNGPVQNPGKSDTNLSDKPTGRWGVGDGFF 217
Qy      237 LLLLGVAGAGGAMC-----WRRRRRAKPSE-----SRHPGPGSFGRGG 273
      : | | | | | : | | : | | : | | : | | : | |
Db      218 NSKIAVFAAIGAGCVIFILIIIFLVLLIKIRKRRKHTQQAALSLSTLASPKCSGNAG 277
Qy      274 SLGLGGGGGMPREAEFGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPQPSP 333
      | | : | | : : | | | | | | | | | | | | | | | | |
Db      278 S-----EPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 320
Qy      334 PNIYY 338
      | | | |
Db      321 ANIYY 325

```

RESULT 11

EFA2\_BRARE

```

ID   EFA2_BRARE          STANDARD;          PRT;   195 AA.
AC   P79727;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1) (ZFEPHL3).
GN   EFNA2 OR EPLG6 OR LERK6.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97195707; PubMed=9043080;
RA   Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U.,
RA   Bonhoeffer F., Holder N.;
RT   "Two Eph receptor tyrosine kinase ligands control axon growth and may
RT   be involved in the creation of the retinotectal map in the
RT   zebrafish.";
RL   Development 124:655-664(1997).
CC   -!- FUNCTION: Control axon growth and may be involved in the creation
CC   of the retino-ectal map.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC   (Potential).
CC   -!- TISSUE SPECIFICITY: Widespread expression in the embryo.
CC   -!- DEVELOPMENTAL STAGE: Expressed in the presumptive midbrain of
CC   developing embryos from the six-somite stage. By 24 hours,
CC   expressed throughout the midbrain including the region of the
CC   presumptive tectum. At later stages, expressed in a graded fashion
CC   throughout the tectum.
CC   -!- SIMILARITY: Belongs to the ephrin family.

```

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DR EMBL; Y09668; CAA70863.1; -.  
 DR ZFIN; ZDB-GENE-990415-66; efna2.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Developmental protein; Neurogenesis; Glycoprotein; Lipoprotein;  
 KW Membrane; GPI-anchor; Signal.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 174 EPHRIN-A2.  
 FT PROPEP 175 195 REMOVED IN MATURE FORM (POTENTIAL).  
 FT DISULFID 57 97 BY SIMILARITY.  
 FT LIPID 174 174 GPI-anchor amidated cysteine (Potential).  
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 195 AA; 22688 MW; 9EE284FEB61D0C42 CRC64;

Query Match 7.6%; Score 185; DB 1; Length 195;  
 Best Local Similarity 29.9%; Pred. No. 1.4e-05;  
 Matches 63; Conservative 21; Mismatches 71; Indels 56; Gaps 7;

Qy 33 VYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC 92  
 |||||:| || :| | : | | ||: || | || | | :| |  
 Db 29 VYWSSNSRFEW-QGEYTVAVSINDYLDVYCPYYESPQPHS--RMERYILFMVNHGDLTC 85  
 Qy 93 EAPPAPNLLLTCDR---PDLDLRFITKFEYSPNLWGHEFRSHHDYIIATSDGTREGLE 149  
 | :| | | | :| | :| | | | :| | | :| |  
 Db 86 EHRMRGFKRWEENRQSPDGPLRFSEKFLFTFSLGFEFRPGHEYYYISSPHPNHAGKP 145  
 Qy 150 SLQGGVCLTRGMKVLRLRVGQSPRGGAVPRKPVSEMPMERDRGAHSLPEPKENLPGDPTS 209  
 | : :| | : || | | | :| | :| |  
 Db 146 CLK-----LKVYV-----KPTSS-----GYESPEPFLTD 169  
 Qy 210 NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240  
 : ||:| | ||:| |  
 Db 170 QSQRCGADGPC-----LAVLML 186

# RESULT 12

## EFA3\_HUMAN

ID EFA3\_HUMAN STANDARD; PRT; 238 AA.  
 AC P52797;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Ephrin-A3 precursor (EPH-related receptor tyrosine kinase ligand 3)  
 DE (LERK-3) (EHK1 ligand) (EHK1-L).  
 GN EFNA3 OR EPLG3 OR LERK3 OR EFL2.



OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95140419; PubMed=7838529;  
 RA Kozlosky C.J., Maraskovsky E., McGrew J.T., Vanden Bos T.,  
 RA Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,  
 RA Cerretti D.P., Beckmann M.P.;  
 RT "Ligands for the receptor tyrosine kinases hek and elk: isolation of  
 RT cDNAs encoding a family of proteins.";  
 RL Oncogene 10:299-306(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95063919; PubMed=7973638;  
 RA Davis S., Gale N.W., Aldrich T.H., Maisonnepierre P.C., Lhotak V.,  
 RA Pawson T., Goldfarb M., Yancopoulos G.D.;  
 RT "Ligands for EPH-related receptor tyrosine kinases that require  
 RT membrane attachment or clustering for activity.";  
 RL Science 266:816-819(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Duodenum;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -!- TISSUE SPECIFICITY: Expressed in brain, skeletal muscle, spleen,  
 CC thymus, prostate, testis, ovary, small intestine, and peripheral  
 CC blood leukocytes.  
 CC -!- SIMILARITY: Belongs to the ephrin family.

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CC      -----
DR      EMBL; U14187; AAC50078.1; -.
DR      EMBL; L37360; AAA52368.1; -.
DR      EMBL; BC017722; AAH17722.1; -.
DR      PIR; I38849; I38849.
DR      Genew; HGNC:3223; EFNA3.
DR      MIM; 601381; -.
DR      GO; GO:0005887; C:integral to plasma membrane; TAS.
DR      GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
DR      GO; GO:0007267; P:cell-cell signaling; TAS.
DR      InterPro; IPR008972; Cupredoxin.
DR      InterPro; IPR001799; Ephrin.
DR      Pfam; PF00812; Ephrin; 1.
DR      PRINTS; PR01347; EPHRIN.
DR      ProDom; PD002533; Ephrin; 1.
DR      PROSITE; PS01299; EPHRIN; 1.
KW      Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
FT      SIGNAL          1      22      POTENTIAL.
FT      CHAIN           23      214     EPHRIN-A3.
FT      PROPEP          215     238     REMOVED IN MATURE FORM (POTENTIAL).
FT      DISULFID        63      110     BY SIMILARITY.
FT      LIPID           214     214     GPI-anchor amidated glycine (Potential).
FT      CARBOHYD        38      38      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        67      67      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD       100     100     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CONFLICT        71      74      MISSING (IN REF. 2).
SQ      SEQUENCE       238 AA; 26350 MW; 8EFD6AE8FE33FDDA CRC64;

Query Match          7.3%; Score 179; DB 1; Length 238;
Best Local Similarity 28.4%; Pred. No. 4.2e-05;
Matches 65; Conservative 24; Mismatches 80; Indels 60; Gaps 12;

Qy      7  GPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCP--R 64
      |||          | ||      :  ||||:|:  : | || :  : | ||: ||
Db      24 GPG-----GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67

Qy      65 ARPPGPHSSP---NYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDL---DLRFTIKF 117
      :  || : |      | | ||:|      | | |      |:||      ::|: ||
Db      68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126

Qy      118 QEYSPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVP 177
      | ||      |:| : |:| | :|      | |      ||| :  :  |
Db      127 QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG--- 174

Qy      178 RKPVSEMP-----MERDRGAAHSLE-----PGKENLP 204
      ||| :|      | :      ||      | :|:|
Db      175 EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223

```

# RESULT 13

## EFA2\_MOUSE

```

ID      EFA2_MOUSE      STANDARD;      PRT;      209 AA.
AC      P52801;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)

```

DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)  
 DE (LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L).  
 GN EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Swiss Webster; TISSUE=Brain;  
 RX MEDLINE=95007776; PubMed=7522971;  
 RA Cheng H.J., Flanagan J.G.;  
 RT "Identification and cloning of ELF-1, a developmentally expressed  
 RT ligand for the Mek4 and Sek receptor tyrosine kinases.";  
 RL Cell 79:157-168(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95181289; PubMed=7876076;  
 RA Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., Dixit V.M.;  
 RT "cDNA cloning and characterization of a Cek7 receptor  
 RT protein-tyrosine kinase ligand that is identical to the ligand  
 RT (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases.";  
 RL J. Biol. Chem. 270:3467-3470(1995).  
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and  
 CC EPHA5.  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor  
 CC (Potential).  
 CC -!- SIMILARITY: Belongs to the ephrin family.  
 CC -----  
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 CC -----  
 DR EMBL; U14941; AAA53636.1; -.  
 DR EMBL; U14752; AAA68520.1; -.  
 DR PIR; A54984; A54984.  
 DR MGD; MGI:102707; Efna2.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 184 EPHRIN-A2.  
 FT PROPEP 185 209 REMOVED IN MATURE FORM (POTENTIAL).  
 FT DISULFID 69 110 BY SIMILARITY.  
 FT LIPID 184 184 GPI-anchor amidated asparagine  
 FT (Potential).  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 209 AA; 23586 MW; F1997545F25B9ABC CRC64;

Query Match 7.2%; Score 176; DB 1; Length 209;  
Best Local Similarity 29.3%; Pred. No. 5.7e-05;  
Matches 58; Conservative 19; Mismatches 69; Indels 52; Gaps 7;

Qy 33 VYWNSANKRFQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87  
| | | | : | | | | | | : | | | | : | | | | |  
Db 35 VYWNRSNPRFQVSAVGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93  
  
Qy 88 QGRRCEAPPAPNLLLTCDRPLD---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGT 144  
| : | : | | | : | | | | : | : | : | :  
Db 94 GHASCDHRQRGFKRWEENRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 151  
  
Qy 145 REGLESLOGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSLEPGKENLP 204  
: | | : | : | | | | | | | | | | | | | | | |  
Db 152 ----PNLVDRPCLR--LKVYVR-----PTNETLY 174  
  
Qy 205 GDP-----TSNATSRGAEG 218  
| | | : | | |  
Db 175 EAPEPIFTSNSSCSGLGG 192

#### RESULT 14

##### EFA2\_HUMAN

ID EFA2\_HUMAN STANDARD; PRT; 213 AA.  
AC O43921; O76020;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)  
DE (LERK-6) (HEK7-ligand) (HEK7-L).  
GN EFNA2 OR EPLG6 OR LERK6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98126446; PubMed=9465306;  
RA Cerretti D.P., Nelson N.;  
RT "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),  
RT mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):  
RT conservation of intron/exon structure."  
RL Genomics 47:131-135(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,  
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,  
RA Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,  
RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,  
RA Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,  
RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,  
RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,  
RA Carrano A.V.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=99045414; PubMed=9826538;  
 RA Aasheim H.C., Pedoutour F., Grosgeorge J., Logtenberg T.;  
 RT "Cloning, chromosomal mapping, and tissue expression of the gene  
 RT encoding the human Eph-family kinase ligand ephrin-A2.";  
 RL Biochem. Biophys. Res. Commun. 252:378-382(1998).  
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and  
 CC EPHA5.  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor  
 CC (Potential).  
 CC -!- SIMILARITY: Belongs to the ephrin family.  
 CC -----  
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 CC -----  
 DR EMBL; U92896; AAC39577.1; -.  
 DR EMBL; U92893; AAC39577.1; JOINED.  
 DR EMBL; U92894; AAC39577.1; JOINED.  
 DR EMBL; AC004258; AAC04896.1; -.  
 DR EMBL; AJ007292; CAA07435.1; -.  
 DR PIR; JE0322; JE0322.  
 DR Genew; HGNC:3222; EFNA2.  
 DR MIM; 602756; -.  
 DR GO; GO:0005106; F:ephrin; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 188 EPHRIN-A2.  
 FT PROPEP 189 213 REMOVED IN MATURE FORM (POTENTIAL).  
 FT DISULFID 73 114 BY SIMILARITY.  
 FT LIPID 188 188 GPI-anchor amidated asparagine  
 FT (Potential).  
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 6 6 R -> A (IN REF. 3).  
 FT CONFLICT 25 26 RA -> PP (IN REF. 3).  
 FT CONFLICT 29 30 AA -> RR (IN REF. 3).  
 SQ SEQUENCE 213 AA; 23878 MW; 33C9FB1A8168B2D0 CRC64;

Query Match 7.2%; Score 175.5; DB 1; Length 213;  
 Best Local Similarity 36.8%; Pred. No. 6.3e-05;  
 Matches 43; Conservative 14; Mismatches 51; Indels 9; Gaps 3;

QY 33 VYWNSANKRFQA-----EGGYVLYPQIGDRDLDCPRARPPGPHSSPNYEFYKLYLVGGA 87  
 |||| :| || | ||| : | | ||: || | | : | | ||:| |  
 Db 39 VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97  
 QY 88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATS 141  
 |: ||| ||: ||| :| | || | :| | : :  
 Db 98 GHASCDHRQRGFKRWEENRPAAPGGPLKFSEKFQLFPSLGFEPGHEYYYISAT 154

RESULT 15

EFA2\_CHICK

ID EFA2\_CHICK STANDARD; PRT; 200 AA.  
 AC P52802;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)  
 DE (LERK-6) (ELF-1).  
 GN EFNA2 OR EPLG6 OR LERK6 OR ELF1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95360981; PubMed=7634327;  
 RA Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.;  
 RT "Complementary gradients in expression and binding of ELF-1 and Mek4  
 RT in development of the topographic retinotectal projection map.";  
 RL Cell 82:371-381(1995).  
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and  
 CC EPHA5 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor  
 CC (Potential).  
 CC -!- TISSUE SPECIFICITY: Expressed in a gradient across the tectum  
 CC being more strongly expressed at the posterior pole.  
 CC -!- SIMILARITY: Belongs to the ephrin family.  
 CC -----  
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 CC -----  
 DR EMBL; L40932; AAC42229.1; -.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 175 EPHRIN-A2.

FT PROPEP 176 200 REMOVED IN MATURE FORM (POTENTIAL).  
 FT DISULFID 61 101 BY SIMILARITY.  
 FT LIPID 175 175 GPI-anchor amidated asparagine  
 FT (Potential).  
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 200 AA; 23049 MW; 8FAB1AE5E45EED96 CRC64;

Query Match 7.0%; Score 172; DB 1; Length 200;  
 Best Local Similarity 35.3%; Pred. No. 0.0001;  
 Matches 49; Conservative 16; Mismatches 58; Indels 16; Gaps 5;

QY 15 ALLLLGVLGLVSGLSLEP-----VYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRA 65  
 | | | : | | | : | | | : | | | : | | | : | |  
 Db 7 AALLAAIVG-VCVWSDDPGKVISDRYAVYWNRSNPRFH-RGDYTVESINDYLDIYCPHY 64  
 QY 66 RPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSP 122  
 | | : | | | : | : | | | : | | : | | : |  
 Db 65 EEPLP--AERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLKFSEKFQLFTP 122  
 QY 123 NLWGHEFRSHHDYIIATS 141  
 | | | | : | | | : |  
 Db 123 FSLGFEFPRPGHEYYYISAS 141

Search completed: September 15, 2004, 12:36:30  
 Job time : 18.7421 secs